Best Available Copy Page 1 us-09-867-159a-2.open.rpr

GenCore VerBion 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM protein - protein search, using sw model	May 19, 2005, 17:16:56 ; Search time 40 Seconds (without alignments) 534.003 Million cell updates/sec	US-09-867-159A-2 ore: 1206 1 TNACSINGNAPAEIDLRQMRYFAANIDLMMIEEYPYVVIL 222
	OM protein - prote	Run on: Ma	Title: US Perfect score: 13 Sequence: 1

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

major fecal allerg carrot seed cystei probable cysteine caricain (EC 3.4.2 caricain (EC 3.4.2 cathepsin L-like p cathepsin K (EC 3. cysteine proteinas cathepsin K (EC 3. oryzain (EC 3.4.22 cysteine proteinas allergen Der p 1 -allergen Der f I p probable cysteine SUMMARIES JN0633 JN0634 JC2276 JC2276 JC2276 JC2276 JC2276 JC227 Query Match Length DB 1144 982.5 389.5 389.5 333.5 322.5 322.5 322.5 322.5 323.5 3 Result

cysteine proteinas	ananain (EC 3.4.22	chymopapain (EC 3.	cysteine proteinas	cysteine proteinas	drought-inducible	cysteine proteinas	cathepsin-like pro	actinidain (EC 3.4	cysteine proteinas	cysteine proteinas	cathepsin L (EC 3.	cysteine proteinas	glycyl endopeptida	cysteine proteinas	cysteine proteinas
T12382	T07839	T09760	T06208	T06529	JN0719	S22502	T30426	S02728	\$49451	T06708	S47433	JQ1121	T09798	T06207	T46630
0	N	7	~	~	~	7	7	~	7	7	7	~	7	~	7
367	345	352	365	367	462	362	356	302	325	361	313	328	348	349	364
25.5	25.5	25.5	25.5	25.5	25.5	25.4	25.3	25.2	25.2	25.2	25.2	25.2	25.1	25.1	25.1
308	307.5	307	307	307	307	306	305.5	304.5	304.5	304.5	304	303.5	303	303	303
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT JQ0337 allerg C,Spec C,Date C,Acce C,Acce R,Con A,Refe A,Refe A,Resi A,Resi A,Trill A,Resi A,	RESULT 1 JUG0337 Jalergen Der D - house-dust mite (Dermatophagoides pteronyssinus) (fragment) C.Species: Dermatophagoides pteronyssinus C.Species: Or-Sep-1990 #sequence revision 07-Sep-1990 #text_change 09-Jul-2004 C.Accession: JUG037, AA7582; Ā31657; C27634 A.Richae. K.Y.; Stewart, G.A.; Thomas, W.R.; Simpson, R.J.; Dilworth, R.J.; Plozza, T.M.; A.A.Cross-men number: JUG037; MUID:88089411; PMID:3335830 A.A.Cross-references: UNIPROT:P08176 A.A.Cross-references: UNIPROT:P08176 A.A.Residues: 1-245 <chu>A.A.Simpson, R.J.; Chua, K.Y.; Plozza, T.M.; Dilworth, R.J.; int. Arch. Allergy Appl. Immunol. 85, 127-129, 1988 A.Fitle: Cloning and expression of DNA coding for the major house dust mite allergen Der A.A.Cress-con. number: A27582; MUID:88114080; PMID:3276629</chu>
A, Mole A, Crosi A, Crosi B, Simp Proteil A, Titl A, Rece A, Rece A, Resle A, Resle A, Resle	A, Molecule type: mRNA A, Molecule type: mRNA A, Essidues: 6-10. THO. 7 THO. A, Cross-references: GB: M24784; NID: 9387591; PIDN: AAA28296.1; PID: 9387592 A, Tailes Structural studies on the allergen Der pl from the house dust mite Dermatophago A, Accession: A31657; MUID: 89098855; PMID: 2911558 A, Status: preliminary A, Molecule type: protein A, Residues: 24-56, XX, 59-64;102-118;134-149;185-192, X', 194-200, X', 202 <sim> E, Lind, P.; Hansen, O.C.; Horn, N.</sim>
J. Imm d by Titl d by Titl d by Refe A; Rese C; Supe C; Keyw F; 24-2;	A. Timnunol. 140, 4256-4262, 1988 A. Title: The binding of mouse hybridoma and human IgB antibodies to the major fecal alle by solid-phase inhibition assays with radiolabeled antigen. A.Reference number: A92819; MVID:88229138; PMID:3372999 A.Accession: C27634 A.Molecule type: protein A.Residues: 24-52 <lin> C.Superfamily: papain C.Superfamily: papain C.Feywords: glycoprotein F.24-245/Product: allergen Der p 1 #status predicted <mat> F.24-245/Product: allergen Carbohydrate (Asn) (covalent) #status predicted</mat></lin>
Query Ma Best Loc Matches	Query Match Best Local Similarity 95.5%; Pred. No. 1.5e-95; Matches 212; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
çy gp	
δλ	61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120

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Page

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Major fecal allergen Der p I - house-dust mite (Dermatophagoides pteronyssinus) (fragment NyAlternate names: allergen Der pl Cippecies: Dermatophagoides pteronyssinus Cippecies: Dermatophagoides pteronyssinus Cipate: 05-War-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004 Cipate: 05-War-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004 Risimpson, R.J.; Nice, B.C.; Moritz, R.L.; Stewart, G.A. Protein Seq. Data Anal. 2, 17-21, 1989 Aritie: Structural studies on the allergen Der pl from the house dust mite Dermatophagon Aritie: Structural studies on the allergen Der pl from the house dust mite Dermatophagon Aritie: Structural studies on the allergen Der pl from the house dust mite Dermatophagon Arities and Structural studies on the allergen Der pl from the house dust mite Dermatophagon Arities and Structural studies on the allergen Der pl from the house dust mite Dermatophagon Arities and Structural studies on the allergen Der pl from the house dust mite Dermatophagon Arities and Structural studies on the allergen Der pl from the house dust mite Dermatophagon Arities and Structural studies on the allergen Der pl from the house dust mite Dermatophagon Arities and Structural studies on the allergen Der pl from the house dust mite Dermatophagon Arities and Structural Stru
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Cispecies: Daucus carota (carrot)
Cispecies: Daucus carota (carrot)
Cispecies: Daucus carota (carrot)
Ciscession: JC7787
Risakuta, C.; Oda, A.; Konishi, M.; Yamakawa, S.; Kamada, H.; Satoh, S.
Biosci. Biosci. Dischem. 65, 2243-2248, 2001
A;Title: Cysteine proteinase gene expression in the endosperm of germinating carrot seeds
A;Reference number: JC7787
A;Contents: Seeds
A;Reference number: JC7787
A;Contents: Seeds
A;Reference number: JC7787
A;Residues: 1-358 <SAK>
A;Residues: 1-358 <SAK>
A;Cross=references: UNIPROT: Q948S1; DDBJ;AB057371; DDBJ;AB057372
C;Comment: This protein is concerned with programmed cell death, and is endosperm-specificies
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                                                                                                                                                                                                                                                                                                                                                                                              59 EQELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQ 118
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                                                                                                                                                                             OELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQI
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Pred. No. 4.2e-28;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 AQGVDYWIVRNSWDTNWGDNGYGYFAANIDL 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: S03380
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28;29-43;44-60;61-76;77-94 <SIM>A;Cross-references: UNIPROT:Q7M431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 IYPPNANK-----
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Best Local Similarity 48.6%;
Matches 88; Conservative (
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C;Superfamily: papain
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#461500
allergen Der f I precursor - house-dust mite (Dermatophagoides farinae)
c;Species: Dermatophagoides farinae
C;Species: Dermatophagoides farinae
C;Date: 07-0ct-1994 #sequence_revision 07-0ct-1994 #text_change 26-Aug-1999
C;Accession: A61500
R;Dilworth, R.J; Chua, K.Y.; Thomas, W.R.
Clin. Exp. Allergy 21, 25-32, 1991
A;Title: Sequence analysis of cDNA coding for a major house dust mite allergen, Der f 1
A;Reference number: A61500; MUID:91215493; PMID:2021874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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84 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 143
                                                                                                                                PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                 144 PPNANKIREALAQPQRYCRHYWTIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 203
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N.Alternate names: allergen Bur m I
C.Species: Euroglyphus maynei must m I
C.Species: Euroglyphus maynei maynei
C.Species: Euroglyphus maynei maynei
C.Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C.Accession: S21864
R.Kent, N.A.; Hill, M.; Keen, J.N.; Holland, P.W.H.; Hart, B.
A.Keference number: S21864
A.Accession: S21864
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A.Accession: L211 *KEN>
A.Reference number: J-211 *KEN>
A.Reference number: J-211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Status: preliminary; not compared with conceptual translation A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-319 < DIL> C; Superfamily: papaily: papaily:
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                                                                                                                                                                                                                                                                                                                                                      204 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 245
                                                                                                                                                                                                                                                                                                         181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 81.5%; Score 982.5; DB 2; Best Local Similarity 83.9%; Pred. No. 4.3e-81; Matches 177; Conservative 17; Mismatches 16;
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C, Superfamily: papain
C, Keywords: cysteine pro
                                                                                                                                121
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A; Molecule type: mRNA
A; Residues: 1-348 <REV>
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A;Residues: 1-348 <STO>
A;Cross-references: UNIPROT:Q92QH7; GB:AE002093; NID:g4314384; PIDN:AAD15594.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable cysteine proteinase [imported] - Arabidopsis thaliana (Species Arabidopsis thaliana (mouse-ear cress) (Species Arabidopsis thaliana (mouse-ear cress) (Species 02-Feb-2001 #text_change 09-Jul-2004 (Species 02-Feb-2001 #text_change 09-Jul-2004 (Spacession: F84672 (Spacession: F8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JN0633
Caricain (EC 3.4.22.30) I precursor - papaya
N;Alternate names: papaya proteinase omega I; peptidase A; peptidase II; proteinase A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84672
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                      GCHGDTIPRGIEYIQHN-GVVQESYYRYVAREQSC--RRPNAQRFGISNYCQIYPPNANK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IREALAQTHSAIAVIIGIKDLDAFRH--YDGRTIIQRDNGYQPNYHAVNIVGY-SNAQGV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : : | : | : | | : : | | : : | | : : | : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : : : : : : : 
LAQAVANQPVSVAIDAGGSDMQFYREGVYTGECGTELD------HGVAVVGYGATNDGT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDNGES---MDWRQEGAVTPVKYQGRCGGCWAFSAVAAVEGITKITKGELVSLSEQQLLD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 CQIYPPNANKIREALAQTHSAIAVIIGIKDLD-AFRHYDGRTIIQRDNGY--QPNYHAVN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -ETVPMNN----EEALLQAVSQQPVSVGIEGTGAAFRHYSGGVF----NGECGTDLHHAVT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDRDYNOGCRGGIMSKAFEYIIKNOGITTEDNYPYQESQOTCSSSTTLSSSFRAATISGY
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                                                                                                                                                                                                                                                                                                                                                                           PAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQELVDCASQH-
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                                                                                                                                                                                                                                                                                          21;
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                                                                                                                                                                                                    27.7%; Score 333.5; DB 2; Length 358; 34.8%; Pred. No. 2.3e-22; ive 36; Mismatches 87; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.5%; Score 332; DB 2; Length 348; 36.2%; Pred. No. 3e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 DYWIVRNSWDTNWGDNGYGYFAANID-----LMMIEEYP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: cscp
C,Superfamily: papain
C,Keywords: cysteine proteinase; hydrolase
F,151,286,307/Active site: Cys, His, Asn #status predicted
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                                                                                                                                                                                                                                               Best Local Similarity 34.8
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84; Conservative
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Matches 84; Conserv
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A;Gene: At2g27420
A;Map position: 2
C;Superfamily: papain
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A, Experimental source: fruit and leaf
R, Dubois, T.; Kleinschmidt, T.; Schnek, A.G.; Looze, Y.; Braunitzer, G.
Biol. Chem. Hoppe-Seyler 369, 741-754, 1988
A;Title: The thiol proteinages from the latex of Carica papaya L. II. The primary struct: A, Reference number: S01135; MID:89105320; PMID:3063283
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N;Alternate names: papaya proteinase omega II
S;Species: Carica papaya (papaya)
C;Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JN0634; A43027; $31823
C;Accession: JN0634; A43027; $31823
A;Revell, D.F.; Cummings, N.J.; Baker, K.C.; Collins, M.E.; Taylor, M.A.J.; Sumner, I.G. A;Title: Mucleotide sequence and expression in Eschericia coli of cDNAs encoding papaya i A;Reference number: JN0633; MUID:93273235; PMID:7684720
C;Species: Carica papaya (papaya)
C;Species: Carica papaya (papaya)
C;Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JN0633; S01135; S11748; A43026; S35728
R;Revell, D.F.; Cummings, N.J.; Baker, K.C.; Collins, M.B.; Taylor, M.A.J.; Sumner, I.G. Gene 127, 221-255, 1993
A;Title: Nucleotide sequence and expression in Eschericia coli of cDNAs encoding papaya A;Reference number: JN0633; MUID:93273235; PMID:7684720
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:P10056; EMBL:X66060; NID:g18097; PIDN:CAA46862.1; PID:g18098
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A;Residues: 1-367 - KBEY.
A;Cross-references: UNIPROT:Q42673; EMBL:X69877; NID:g22660; PIDN:CAA49504.1; PID:g22661
A;Experimental source: fruit and leaf
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A;Residues: 133-348 «DUB»
R;Collins, M.E.; Revell, D.F.; Sumner, I.G.; Pickersgill, R.W.; Goodenough, P.W.
Submitted to the EMBL Data Library, February 1990
A;Reference number: S11748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 SHGCKGGYPPYALEYVAKNGIHLRSKYPYKAKQGTCR---AKQVGGPIVKTSGVGRVQPN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 NEGNLIANAIAK--QPVSVVVESKG-RPFQLYKG-GIFEGPCGTKVD-HAVTAVGYGKSGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 NANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQG 182
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C;Genetics:
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C;Keywords: cysteine proteinase; hydrolase
F;1-14/Domain: signal sequence #status predicted <SIG>
F;15-132/Domain: propeptide #status predicted <PRO>
F;13-348/Product: caricain #status experimental <MAT>
F;134-195,188-227,285-336/Disulfide bonds: #status predicted
F;157,291,311/Active site: Cys, His, Asn #status predicted
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304 KGYILIKNSWGTAWGEKGY 322
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A;Residues: 237-348 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 NEGNILNAIAK--QPVSVVVESKG-RPFQLYKG-GIFEGPCGTKVD-HAVTAVGYGKSGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 PESIDWRDYYYVTEVKDÓGÓGGSCWAFSTTGAVEGOFRKNERASASFSEGOLVDCTRDFG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 QHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFG-ISNYCQIYPPNANK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 IREALAQTHSAIAVIIGIKDLDAFR-HYDGRTIIQRDNGYQPN-----YHAVNIVGYS 178
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A,Residues: 1-236 <HEU>
A,Crose-references: UNIPROT:Q24944; EMBL:Z22765; NID:g452257; PID:g452258
C,Superfamily: papain
C,Keywords: cysteine proteinase; hydrolase
F;132,269,289/Active site: Cys, His, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
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                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indele
A Gene: Pp-omega
C; Superfamily: papain
C; Superfamily: papain
C; Superfamily: papain
C; Superfamily: papain
C; Silly Domain: aginal sequence #status predicted <PRO>
F; 12-132/Domain: propeptide #status predicted <PRO>
F; 13-357/Product: caricain II #status predicted <PMI>
F; 154-195, 188-227, 285-336/Disulfide bonds: #status predicted
F; 157, 291, 311/Active site: Cys, His, Asn #status predicted
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A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                   Score 327; DB 2;
Pred. No. 9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 SQDGTDYWIVKNSWGTWWGEDGYIRFARN 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 KGYILIKNSWGTAWGEKGY 322
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 37.2%;
Matches 74; Conservative 3.
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Matches 72; Conservative
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RESULT 10

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cathepsin K (EC 3.4.22.-) precursor - human

NyAlternate names: cathepsin O2

C,Species: Homo sapiens (man)

C,Species: Homo sapiens (man)

C,Species: Homo sapiens (man)

C,Species: Homo sapiens (man)

C,Species: Lieb-1995 #sequence revision 05-Apr-1995 #text_change 09-Jul-2004

C,Accession: JC2476; S55763; S68459; I38752; S48830

R,Indacka, T.; Bilbe, G.; Ishibashi, O.; Tezuka, K.; Kumegawa, M.; Kokubo, T.

Biochem. Biophys: Res. Commun. 206, 89-96; 1985

A;Title: Molecular cloning of human cDNA for cathepsin K: Novel cysteine proteinase predct A;Reference number: JC2476; MUID:95118380; PMID:781855

A;Accession: JC2476

A;Molecule type: mRNA

A;Reference number: Seyler 376, 379-384, 1995

A;Title: Human cathepsin O2, a novel cysteine protease highly expressed in osteoclastomate A;Reference number: S55763; MUID:96082523; PMID:7576232

A;Status: preliminary

A;Residues: J229 BRO>

A;R
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C;Species: Nicotiana tabacum (common tobacco)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T03941
R;Becker, C; Muentz, K.
abbacker, C; he EMBL Data Library, September 1997
A;Description: CDNA cloning of a CPR1-homologous proteinase from germinating tobacco seec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: GB:S79895; NID:g1195555; PIDN:AAB35521.1; PID:g1195556
R;Shi, G.P.; Chapman, H.A.; Bhairi, S.M.; DeLeeuw, C.; Reddy, V.Y.; Weiss, S.J.
FEBS Lett. 357, 129-134, 1995
A;Title: Molecular cloning of human cathepsin O, a novel endoproteinase and homologue of A;Reference number: 138752; MUID:95104457; PMID:7805878
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A; Residues: 1-329 cKH:>
A; Residues: 1-329 cKH:>
A; Residues: 1-329 cKH:>
A; Residues: 1-320 cKH:>
A; Residues: 1-320 cKH:>
A; Experimental source: tissue-type blood
C; Genetics:
A; Gene: GDB:CTSK; PYCD; CTSO1; CTSO2; PKND; CTSO
A; CTOSB-references: GDB:453910; OMIM:265800; OMIM:600550; OMIM:601105
C; Superfamily: papain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 329;
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Local Similarity 36.0%; Pred. No. 1.6e-21;
he 73; Conservative 30; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :||::||| |||: ||
291 HWIIKNSWGENWGNKGYILMARN 313
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A;Cross-references: UNIPROT:P12412; EMBL:X51900; NID:g22065; PIDN:CAA36181.1; PID:g22066 R;Akasofu, H.; Yamauchi, D.; Mitsuhashi, W.; Minamikawa, T. Nucleic Acids Res. 17, 6733, 198 A;Afitle: Nucleic Acids Res. 17, 6734, 198 A;Afitle: Nucleotide sequence of CDNA for sulfhydryl-endopeptidase (SH-EP) from cotyledon A;Reference number: S05497; MUID:89386007; PMID:2780300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: protein
A,Residue8: 132-140 <AKA3>
A;Residue8: 132-140 <AKA3>
Fichamoto, T.; Nakayama, H.; Seta, K.; Isobe, T.; Minamikawa, T.
FEBS Lett. 351, 31-34, 1994
A;Title: Posttranslational processing of a carboxy-terminal propeptide containing a KDEL
A,Reference number: $48684; MUID:94357273; PMID:8076688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mungo sulfhydryl-endopeptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 NANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGY-SNAQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 GNAPABIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQELVDCAS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cysteine proteinase (EC 3.4.22.-) precursor - black gram N;Alternate names: cysteine endopeptidase; sulfhydryl endopeptidase C;Species: Vigna mungo (black gram) C;Species: Vigna mungo (black gram) 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: S12581; S05497; $20213; S48684 R;Akasofu, H.; Yamauchi, D.; Minamikawa, T. Nucleic Acids Res. 18, 1892, 1990 A;Fitle: Nucleotide sequence of the gene for the Vigna mungo sulfhydryl-endo A;Fitle: Nucleotide sequence of the gene for the Vigna mungo sulfhydryl-endo A;Reference number: S12581; MUID:90245586; PMID:2336365
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A;Accession: S20213
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                                                                                                                                                                                                                                                                        321
                                                                                                                                                                                                    154 DGRTIIQRDNGYQPNYHAVNIVGY-SNAQGVDYWIVRNSWDTNWGDNGY 201
                                                        AREQSCRRPNAQRFGISNYCQIYPPNANKIREALAQTHSAIAVIIGIKDLDA
                                                                                                                                                                                                                                          274 SGGVYNARNCGTSVN-HAVTLVGYGTSPEGMKYWLAKNSWGKTWGENGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: cysteine proteinase; hydrolase
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-362/Product: cysteine proteinase #status predicted <MAT>
F;152,288,309/Active site: Cys, His, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVDYWIVRNSWDTNWGDNGYGYFAANID-----LMMIEEYP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.7%; Score 322; DB 1; 35.0%; Pred. No. 2.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: protein
A,Residues: 127-140;197-216;324-333;339-352 <OKA>
C,Genetics:
A;Introns: 150/1; 228/3; 275/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-362 <AKAl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-362 <AKA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: S05497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: S48684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S12581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78;
                                                        98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cysteine proteinase (EC 3.4.22.-) [similarity] - Arabidopsis thaliana (cysteine proteinase (EC 3.4.22.-) [similarity] - Arabidopsis thaliana (cysteine proteinase (EC 3.4.22.-) [similarity] - Arabidopsis thaliana (cysteine or arabidopsis thaliana (mouse-ear cress) [cysteine or ara-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 [cycession: C8641] [cysteine] [c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGCHGDTIPRGIEYIQHNGVVQ-ESYYRYVAREQSCR--RPNAQRFGISNYCQIYPPNAN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQGVDY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGLRGVNVTSPFEVVNETKPAWNWTVSDVLGTNKDWRNEGAVTPVKSQGECGGCWAFSAI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 AAVEGLTKIARGNLISLSEQQLLDCTREQNNGCKGGTFVNAFNYIIKHRGISSENEYPYQ 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 PAEIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDC--ASO 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATESAYLAHRNQSLDLAEQELVDCASQ--HGCHGDTIPRGIEY-IQHNGVVQESYYRYV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---- DLROMRTVTPIRMOGGCGSCWAFSGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 374;
A;Reference number: Z15148
A;Accession: T03941
A;Statuse: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-374 <BEC>
A;Residues: 1-374 <BEC>
A;Residues: 1-374 <BEC>
A;Cross-references: UNIPROT:024137; EMBL:299173; PIDN:CAB16317.1
A;Experimental source: clone TCPR1
C;Superfamily: papain
C;Superfamily: sayanl sequence #status predicted <SIG>
F;1-20/Domain: signal sequence #status predicted <MAT>
F;11-374/Product: cysteine proteinase #status predicted <MAT>
F;164,239,319/Active site: Cys, His, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 322; DB 2; Length 346;
; Pred. No. 2.4e-21;
33; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Superfamily: papain
C:Keywords: cysteine proteinase; hydrolase
F:154,289,310/Active site: Cys, His, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WIVENSWGTKWGENGYVKMERNVKKSHLGKCGIMTEASYP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.7%; Score 322.5; DB 2
36.8%; Pred. No. 2.3e-21;
cive 28; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.7%; Score 322; 32.3%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TNACSINGNAPAEI ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 36.8
1es 81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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254 VNNEKALQKAVAHQPVSIALEAGGRD---FQHYKSGIFTGKCGTAVD------HGVVIA 303
121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHY-----DGRTIIQRDNGYQPNYHAVNIV 175
                                                                                                                                                                                                            304 GYGTENGMDYWIVRNSWGANWGENGY 329
                                                                                                                                                             176 GYSNAQGVDYWIVRNSWDTNWGDNGY
                                                                                                                                                                                                                                                                                                                                                                Search completed: May 19, 2005, 17:23:28 Job time: 41 secs
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                                                                                                                                                                                                                                         g
                     Cysteine proteinase (EC 3.4.22.-) precursor - spring vetch C;Species: Vicia sativa (spring vetch, tare) C;Accession: S51817; S47312 C;Accession: S51817; S47312 1994 M.H.; Muenitz, K. R;Becker, C.; Fischer, J.; Nong, V.H.; Muenitz, K. Plant Wol. Biol. 26, 1207-1212, 1994 M.H.; Mulb: Plant Wol. Biol. 26, 1207-1212, 1994 M.H.; Mulb: Plant Wol. Biol. 26, 1207-1212, 1994 M.H.; Mulb: Plant Wol. Biol. 26, 1207-1212, Mulb: Plant Wol. A;Reference number: S51817; Mulb: P5111103; PMID: 7811978 M.H.; Mulb: Pill: Mulb: Pill: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --ASQHGCHGDTIPRGIEY-IQHNGVVQESYYRYVAREQSC--RRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 HGCHGDTIPRGIEYIQHNGVVQ-ESYYRYVAREQSC--RRPNAQRFGISNYCQIYPPNAN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 EGCNGGLMDYAFEFIIGNGGIDTDOHÝPÝKGFEGRCDPTŘKKÁKIVSÍDGÝEDVPSNNEN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIREALAQTHSAIAVIIGIKDLDAFRH--YDGRTIIQRDNGYQPNYHAVNIVGYSNAQGV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 VGDSLPESIDWREKGVLVGVKDQGSCGSCWAFSAVAAMESINAIVTGNLISLSEQELVDC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 PAEIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDC--ASQ 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cysteine proteinase (EC 3.4.22.-) precursor - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A, Residues: 1-466 < LER.>
A, Cross-references: UNIPROT: 049877; EMBL: AJ003137; PIDN: CAA05894.1
A, Experimental source: cultivar Cherry
C, Genetics:
A, Gene: C14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.6%; Score 321; DB 2; Length 368; Best Local Similarity 35.1%; Pred. No. 3.1e-21; Matches 72; Conservative 34; Mismatches 85; Indels 1
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C;Keywords: cysteine proteinase; hydrolase
F;162,298,318/Active site: Cys, His, Asn #status predicted
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R'Lers, A.
R'Lers, A.
R'Accession: T06416
A'Reference number: 215662
A'Accession: T06416
A'Status: preliminary; translated from GB/EMBL/DDBJ
A'Molecule type: mRNA
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Compugen Ltd.
 GenCore version (c) 1993 - 2005
              Copyright
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OM protein - protein search, using sw model

Run on:

May 19, 2005, 17:13:36 ; Search time 60 Seconds (without alignments) 1894.693 Million cell updates/sec

US-09-867-159A-2

1206 1 TNACSINGNAPAEIDLRQMR.....YFAANIDLMMIEEYPYVVIL 222 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 DB seq Minimum E Maximum E

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* .. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

	Description	P08176 dermatophag	P25780 euroglyphus	P16311 dermatophag	Q9gyy0 dermatophag	Q95x05 dermatophag	Q8i9pl psoroptes o	Q95x04 dermatophag		_	Q95pj4 blomia trop	Q7sxq7 petromyzon		Q9zqh7 arabidopsis	Q717s6 callosobruc	Q6e7b4 brugia mala		Q7xyu7 anthurium a	Q7x7a6 glycine max	017473 brugia paha	carica	-	fasciol	Q6qxf0 agrotis seg	_	Q71789 callosobruc		Q717t0 callosobruc	Q9xf79' sandersonia	P43235 homo sapien	P61276 macaca fasc	
SUMMAKIES	QI	MMAL DERPT	EUM1_EURMA	MMAL_DERFA	Q9GY <u>Y</u> 0	Q95X05	Q819P1	Q95X04	Q968Y3	Q7M431	Q95PJ4	Q7SXQ7	64HZ9O	24ÖZ6Ö	Q717S6	Q6E7B4	Q6T857	Q7XYU7	Q7X7A6	CATL_BRUPA	PAP3_CARPA	042673	Q24944	Q6QXF0	Q717S5	071789	90NC70	Q717T0	Q9XF79	CATK HUMAN	CATK MACFA	
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* Query	Match	99.2	86.0	82.7	78.3	50.3	49.0	38.9	36.2	32.3	31.7	28.3	27.6	27.5	27.4	27.4	27.2	27.2	27.2	27.2	27.1	27.1	27.1	27.1	27.0	26.9	26.9	26.9	26.9	26.8	26.8	
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06fhn2 homo sapien 086gf7 pandalus bo 0717s1 callosobruc 093xq9 ipomoea bat 0717s4 callosobruc 09mw2 fasciola gi 024137 nicotiana t 07yx13 tenebrio mo 091p39 arabidopsis P12412 vigna mungo	Q41696 vicia sativ Q9bjm2 litomosoide O49877 lycopersico
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ALIGNMENTS

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SEQUENCE FROM N.A., AND POLYMORPHISM.
MEDLINE=93857682; PubMed=8353459;
Chua K.Y., Kehal P.K., Thansa W.R.;
"Sequence polymorphisms of cDNA clones encoding the mite allergen Der
                                                             P08176; Q24616;
01-AUG-1988 (Rel. 08, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Major mite fecal allergen Der p 1 precursor (EC 3.4.22.-) (Der p 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88114080; PubMed=3276629; Thomas W.R., Stewart G.A., Simpson R.J., Chua K.Y., Plozza T.M., Dilworth R.J., Nisbet A., Turner K.J.; Chua K.Y., Plozza T.M., Dilworth R.J., Nisbet A., Turner K.J.; "Cloning and expression of DNA coding for the major house dust mite allergen Der p I in Escherichia coli."; Int. Arch. Allergy Appl. Immunol. 85:127-129(1988).
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SEQUENCE OF 99-308 FROM N.A.
MEDILINE-93130112; PubMed-1483062;
Kent N.A., Hill M.R., Keen J.N., Holland P.W., Hart B.J.;
"Molecular characterisation of group I allergen Eur m I from house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88089411; PubMed=3335830; Chua K.Y., Stewart G.A., Thomas W.R., Simpson R.J., Dilworth R.J., Plozza T.M., Turner K.J.; "Sequence analysis of cDNA coding for a major house dust mite allergen, Der pl. Homology with cysteine proteases."; J. Box. Med. 167:175-182(1988).
                                                                                                                                                                                                                                                              Dermatophagoides pteronyssinus (House-dust mite).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
Pyroglyphidae; Dermatophagoides.
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MEDLINE=91215493; PubMed=2021874;
Dilworth R.J., Chua K.Y., Thomas W.R.;
"Sequence analys of CDNA coding for a major house dust mite allergen, Der f I.";
Clin. Exp. Allergy 21:25-32(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Int. Arch. Allergy Immunol. 101:364-368(1993).
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Int. Arch. Allergy Immunol. 99:150-152(1992)
                                  320 AA.
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SEQUENCE OF 99-127.
MEDLINE-88229138; PubMed=3372999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALLERGEN: Causes an allergic reaction in human. Common symptoms of mite allergy are bronchial asthma, allergic rhinitis and conjunctivitis. Reacts with IgE in 80% of patients with house dust
                                                                                                                                                                                                  SEQUENCE OF 99-139; 177-192; 208-224 AND 260-277, AND VARIANT ALA-222
Lind P., Hansen O.C., Horn N.;
"The binding of mouse hybridoma and human IgE antibodies to the major fecal allergen, Der p I, of Dermatophagoides pteronyssinus. Relative binding site location and species specificity studied by solid-phase inhibition assays with radiolabeled antigen.";
J., Immunol. 140:4256-4262(1988).
                                                                                                                                                                                                                     Pubmed=2911558;
Simpson R.J., Nice E.C., Moritz R.L., Stewart G.A.;
"Structural studies on the allergen Der pl from the house dust mite
Dermatophagoides pteronyssinus: similarity with cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Comparative modelling of major house dust mite allergen Der p I: structure validation using an extended environmental amino acid propensity table.";
Protein Eng. 7:869-894(1994).
-!- FUNCTION: This. protease that hydrolyzes proteins, with a preference for Phe or basic residues.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000169; Pept_cys acsite.
InterPro; IPR000169; Pept_dase_C1.
InterPro; IPR00125; Peptidase_C1.
InterPro; IPR00159; Peptidase_C1; I.
PRINTS; PR00159; Peptidase_C1; I.
SMART; SN00645; Pept_C1; I.
PROSITE; PS00139; THIOL_PROTEASE_CYS; I.
RPOSITE; PS00649; THIOL_PROTEASE_CYS; I.
RAllergen; Direct protein sequencing; Glycoprotein; Hydrolase; Is Polymorphism; Signal; Thiol_protease; Zymogen.
I SIGNAL
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Major mite fecal allergen Der p 1.
N-linked (GlCNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95062135; Pubmed=7971950;
Topham C.M., Srinivasan N., Thorpe C.J., Overington J.P.,
Kalsheker N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AOBIF4DD09791DFE CRC64;
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Y -> H.
Y -> A.
Y -> A.
S -> T.
E -> Q.
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EMBL; M24794; AAA28296.1; ALT_INIT.
EMBL; X65197; CAA46317.1; -.
PIR; JQ0337; JQ0337.
PISSP; P53634; IX3B.
MEROPS; C01.073; -.
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or send an email to license@lsb-sib.ch).
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                                                                                                                                                             61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
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MEDLINE=99126275; PubMed=9925958; DOI=10.1159/000024026;
Smith W., Mills K., Hazell L., Hart B.J., Thomas W.;
"Molecular analysis of the group 1 and 2 allergens from the house dust
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dust mite Euroglyphus maynei.";
Int. Arch. Allergy Immunol. 99:150-152(1992).
-!- FUNCTION: Probable thiol protease.
-!- SUBCELLULAR LOCATION.
-!- ALLERGEN: Causes an allergic reaction in human. Common symptoms of mite allergy are bronchial asthma, allergic rhinitis and
                                                                                                                                                                                       159 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY
                                                                                  1 TNACSINGNAPAEIDLROMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
                                                                                                         99 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAYRNQSLDLAEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUM1_EURMA STANDARD;
PS2780; Q9TZ23; Q9TZ4; Q9UBA0;
01-MAY-1992 (RR1. 22, Carta, 22)
16-OCT-2001 (Rel. 46, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Mite group 1 allergen Eur m 1 precursor (EC 3.4.22.-) (Eur m I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euroglyphus maynei (Mayne's house dust mite).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
Pyroglyphidae; Euroglyphus.
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  Length 320,
                                          Indels
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  Score 1196; DB 1;
Pred. No. 4.9e-99;
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Int. Arch. Allergy Immunol. 118:15-22(1999)
                                          1; Mismatches
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EMBL; AF047611; AAC82352.1; ALT_INIT.
EMBL; AF047612; AAC82353.1; -.
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  Query Match
Best Local Similarity 99.1'
Matches 220; Conservative
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HSSP; P53634; 1K3B.
MEROPS; C01.073; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYACSINSVSLPSELDLRSLRTVTPIRMQGGGSCWAFSGVASTESAYLAYRNMSLDLAE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QELVDCASQNGCHGDTIPRGIEYIQQNGVVQEHYYPYVAREQSCHRPNAQRYGLKNYCQI 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 SPPDSNKIRQALTQTHTAVAVIIGIKDLNAFRHYDGRTIMQHDNGYQPNYHAVNIVGYGN 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 YPPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNACSING-NAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-FBB-1995 (Rel. 31, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Major mite fecal allergen Der f l precursor (BC 3.4.22.-) (Der f I).
                                                    ProDom; PD00158; Peptidase_C1; 1.
SWART; SM00645; Pept_C1; 1.
PROSITE; PS00640; THIOL_PROTEASE_RSN; 1.
PROSITE; PS00139; THIOL_PROTEASE_HIS; 1.
Allergen; Glycoprotein; Hydrolase; Signal; Thiol protease; Zymogen.
SIGNAL 1 18 Potential.
PROPEP 9 321 Mite group 1 allergen Bur m 1.
AT_SITE 133 133 By similarity.
ACT_SITE 269 269 By similarity.
DISTLEID 130 170 By similarity.
                                                                                                                                                                                                        Mite group 1 allergen Bur m 1.

By similarity.
By similarity.
By similarity.
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
T -> S (in Eur m 1.0102).
M -> I (in Eur m 1.0102).
M -> I (in Eur m 1.0102).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dermatophagoides farinae (House-dust mite).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
Pyroglyphidae; Dermatophagoides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                               86.0%; Score 1037.5; DB 1; Length 321; 83.9%; Pred. No. 8.4e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a major house dust mite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 AQGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TQGVDYWIVRNSWDTTWGDNGYGYFAANINLMMIEQYPYVVML 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kent N., Hill M.R., Keen J.N., Holland P.W., Hart B.J.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                         6CFD44FEC725999E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dilworth R.J., Chua K.Y., Thomas W.R.; "Sequence analysis of cDNA coding for
InterPro, IPR000668, Peptidase_Cl.
Paran, PP00112, Peptidase_Cl, 1.
PRINTS, PR00705, PAPAIN.
ProDom, PD000158; Peptidase_Cl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clin. Exp. Allergy 21:25-32(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88229138; PubMed=3372999;
Lind P., Hansen O.C., Horn N.;
                                                                                                                                                                                                                                                                                                                                                                                                           36290 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 98-309 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 83.9
Matches 187; Conservative
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P16311;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibe.sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000169; Pept cys_acsite.
InterPro; IPR000669; Peptidase_C1.
Pfam; PF00112; Peptidase_C1; 1.
PR00176; PRADAIN.
ProDom; PD000158; Peptidase_C1; 1.
ProDom; P0000158; Peptidase_C1; 1.
PROSITE; PS000649; PHIOL.PROTEASE ASN; 1.
PROSITE; PS000649; THIOL.PROTEASE TYS; 1.
PROSITE; PS00639; THIOL.PROTEASE HIS; 1.
Allergen; Direct protein sequencing; Glycoprotein; Hydrolase; Signal; Thiol protease; Zymogen.
I 18 Potenrial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QELVDCASQHGCHGDTIPRGIEYIQQNGVVEERSYPYVAREQRCRRPNSQHYGISNYCQI
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"The binding of mouse hybridoma and human IgE antibodies to the major fecal allergen, Der p I, of Dermatophagoides pteronyssinus. Relative binding site location and species specificity studied by solid-phase inhibition assays with radiolabeled antigen.";
J. Immunol. 140.4256-4262(1988).
-:-FUNCTION: Thiol protease that hydrolyzes proteins, with a preference for Phe or basic residues.
-:-SUBCELLULAR LOCATION: Secreted.
-:-SUBCELLULAR LOCATION: Secreted.
-:-ALLERGEN: Causes an allergic reaction in human. Common symptoms o mite allergy are bronchial asthma, allergic rhinitis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.7%; Score 997.5; DB 1; Length 321; 81.2%; Pred. No. 3.3e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential.
Activation peptide.
Major mite fecal allergen Der f
By similarity.
By similarity.
N-linked (GlCNAC. . .) (Potentia
By similarity.
By similarity.
By similarity.
By similarity.
C - 0 (in Ref. 2).
D - > V (in Ref. 2).
W, 04523E54EEBB476E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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    -!- SIMILARITY: Belongs to the peptidase C1 family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X65196; CAA46316.1; -.
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Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A27634; A27634.
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MEROPS; C01.073; -.
                                                                                                                                                                                                                                                                                                            conjunctivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 AA;
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61 REQQCRRPNSQHYGISNYCQIYPPDVKQIREALTQTHTAIAVIIGIKDLRAFQHYDGRTI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 REOSCRRPNAORFGISNYCQIYPPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 LVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIYP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIEYIQQNGVVEERSYPYVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 GVAATESAYLAHRNQSLDLAEQELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 ACSING-NAPABIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQE
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Psoroptes ovis (Sheep scab mite).

Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Sarcoptoidea;

Psoroptidae; Psoroptes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 263;
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GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; Peptidase_C1.
Pfam; PF00112; Peptidase_C1; 1.
ProDom; PD000158; Peptidase_C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                     Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Indels
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MEDLINE=22294898; PubMed=12406195;
Liee A.J., Machell J., Van Den Broek A.H.M., Nisbet A.J.,
Miller H.R.P., Isaac R.E., Huntley J.F.;
"Identification of an antigen from the sheep scab mite,
ovis, homologous with house dust mite group I allergens.
Parasite Immunol. 24:413-422 (2002).
EMBL; AF495854; AAO14671.1; -..
HSSP; P14080; 1YAL.
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                                                                                                                                                                                                                                                                      146 146
146 AA; 16852 MW; BB304800946D4047 CRC64;
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                       HSSP, P43235, 1BY8.
GO: GO:0008234; F:cysteine-type peptidase activity;
GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
INTEPERO, IPR000668; Peptidase CI.
PFoull2; Peptidase CI: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                 Score 607; DB 2;
Pred. No. 1.5e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 64.4%; Pred. No. 7.2e-
Matches 112; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 84.2%;
Matches 112; Conservative
EMBL; AF194431; AAL:14424.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 IQRDNGYQPNYHA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 IQHDNGYQPNYHA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SACRINSVAVPSELDLRSLRTVTPIRMQGGGSCWAFSGVAATESAYLAYRATSLDLSEQ 60
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                                                                                                                                                                              Allergen Der fi (Fragment).
Dermatophagoides farinae (House-dust mite).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea; Pyroglyphidae; Dermatophagoidee.
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Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
Pyroglyphidae; Dermatophagoides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hao M.Q., Xu J., Zhong N.S.;

L Submitted (JuL-2000) to the EMBL/GenBank/DDBJ databases.

L-1-SIMILARITY: Belongs to peptidase family Cl.

EMBL, AR783763; AAG00520.1; -..

R PIR; A27634; A27634

R HSSP; P80067; 1JQP.

R GO; GO:0004197; F:veyteine-type endopeptidase activity; IEA.

GO; GO:000508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR000668; Peptidase_Cl.

R InterPro; IPR000689; Peptidase_Cl.

R InterPro; PR000159; Peptidase_Cl.

R PROSITE; PS00040; THIOL_PROTEASE ASN; 1.

R PROSITE; PS00640; THIOL_PROTEASE ASN; 1.

R PROSITE; PS00639; THIOL_PROTEASE HS; UNCNOWN_1.

R PROSITE; PS00639; THIOL_PROTEASE HS; UNCNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Park H., Park S.K., Yun H.C.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 AA; 23548 MW; BA08029D642EEB90 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OGVDYWIVRNSWDTNWGDNGYGYFAANIDL 210
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210 AA
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PRELIMINARY;
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Query Match
Best Local Simil
Matches 81; C
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150 LVDCASQHGCGGDTVLNGLRYIQKNGVVEEQSYPYKAREGRCQRPNAKRYGIKDLCQIYP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 PRGIEYIQQNGVVEERSYPYVAREQQCRRPNSQHYGISNYCQIYPPDVKQIREALTQTHT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                          PNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIV 175
                                                              Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea; Pyroglyphidae; Dermatophagoides.
NCBI_TaxID=6954;
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Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
Pyroglyphidae; Dermatophagoides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 AIAVIIGIKOLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQGV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 469; DB 2; Length 10
Pred. No. 2.5e-34;
8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Park H., Park S.Y., Kim K.Y., Park S.K., Yun H.C.;
Submitred (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF194432; AAL14425.1; -..
Interpro; IPR000169; Pept cyg acsite.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; CO1.073; -.
GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
GO; GO:0006503; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000668; Peptidase_Cl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Park H., Yun H.C., Kim K.Y., Park S.Y., Park S.K.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF145247; AAK38773.1; -.
HSSP; P60994; 1IWD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 107
107 AA; 12277 MW; A80E7876CBA6F97A CRC64;
                                                                                                                                                                                                                             (TrEWBLrel. 19, Created)
(TrEWBLrel. 19, Last sequence update)
(TrEWBLrel. 26, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                            107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 AA
                                                                                                                                                                                                                                                                                                                                              Dermatophagoides farinae (House-dust mite).
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                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                 Cysteine proteinase (Fragment).
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1 Similarity 80.4%;
86; Conservative 8
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                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                Q95X04;
01-DEC-2001 (TrEMBLrel
01-DEC-2001 (TrEMBLrel
01-MAR-2004 (TrEMBLrel
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01-DEC-2001
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SEQUENCE
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                                                                                                                                               RESULT 10095XQ4 10095XQ4 10095XQ4 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10095 10
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                                                                                                                                                                                                                                                                 61 EQAYEYNARENNCEPPENPRHSIEQYCQIDHSNVELIKTALDKYKSAVAVIINIHNINAF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 IYPPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYS 178
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                                                                                                                                                1 CGSCWAFAGVAAVESAYLAFRNQSINLAEQELVDCAARRGCHGDTIPRGLDYIQQNGIVE
                                                                                                                   31 CGSCWAFSGVAATESAYLAHRNQSLDLAEQELVDCASQHGCHGDTIPRGIEYIQHNGVVQ
                                                                                                                                                                                                                                ESYYRYVAREQSCRRPNAQRFGISNYCQ1YPPNANKIREALAQTHSAIAVIIGIKDLDAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TNACSINGNAPAEIDLROMRIVIPIR -- MOGGCGSCWAFSGVAATESAYLAHRNQSLDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 INACSINGNAPAEIDLROMRIVIPIRMOMOGGCGSXXAFSGVA-------
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89098855; PubMed-2911558; Simpson R.J., Stewart G.A.; Simpson R.J., Nice E.C., Moritz R.L., Stewart G.A.; Structural studies on the allergen Der pl from the house dust mite Dermatophagoides pteronyssinus: similarity with cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dermatophagoides pteronyssinus (House-dust mite).

Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
Pyroglyphidae; Dermatophagoides.
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     Length 133;
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 AA; 10327 MW; 9BF744165C8428A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein Seq. Data Anal. 2:17-21(1989).

PIR, S03380, S03380.

G0, G0:0008234; F:cysteine-type peptidase activity;

G0, G0:000508; P:proteolysis and peptidolysis; IEA.

InterPro. IPR000668; Peptidase_C1.

ProDom; PD000158; Peptidase_C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Major fecal allergen Der p I (Fragments).
36.2%; Score 437; DB 2;
llarity 61.4%; Pred. No. 2.4e-31;
Conservative 17; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarior
nes 88; Conservative
                                                                                                                                                                                                                                                                                                                                           151 RHYDGRTIIQRD 162
                                                                                                                                                                                                                                                                                                                                                                                                   121 RHYDGSYVITTD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Length 333;

Indels

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69 H---GCHGDTIPRGIEY-IQHNGVVQESYYRYVAREQSCR-RPNAQRFGISNYCQIYPPN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 ANK--IREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 YYNNGCNGGRSERALQYIDDNGIDSELSYPYEHADGKCRFKPANVATKCSSY-QFVEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 NAPAEIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDCASO
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
Uinuk-ool T.S., Takezaki N., Kuroda N., Figueroa F., Sato A., Samonte I.E., Mayer W.E., Klein J.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AY333299; AAQ01146.1; -. HSSP; P25774; IGLO.
                                                                                                                                                                                   GO, GO:0004197; F:cysteine-type endopeptidase activity; IEA. GO; GO:0005508; P:proteolysis and peptidolysis; IEA. InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; Peptidase_C1.
Probom; PD00112; Peptidase_C1; 1.
Probom; PD00118; Peptidase_C1; 1.
SWART; SW00645; Pept_C1; 1.
SROUENCE 333 AA; 37500 MW; OB0D129A74BB099A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2,
clone:031191 GO8.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family C1.
EMBL; AP004047; BAD09165.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 GVDYWIVRNSWDTNWGDNGYGYFAANID----LAMMIEEYPYV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 GNDFWIVKNSWGEDWGEKGYIYMIRNKDNOCGIASIGIYPII 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IRR000668; Peptidase CI. InterPro; IRR000669; Peptidase CI. InterPro; IRR000169; Pept cys_acsite. Pfam; PF00112; Peptidase CI; I. PRINTS; PR000158; Peptidase CI; I. SMART; SM00645; Pept CI; I. SMART; SM06640; THIOL PROTEASE ASN; I. PROSITE; PS00640; THIOL PROTEASE CY; I. Hydrolase; Protease; Thiol protease. SEQUENCE 366 AA; 40600 MW; 89529D2315608C4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.3%; Score 341.5; DB 2
Best Local Similarity 36.0%; Pred. No. 2.6e-22;
Matches 80; Conservative 36; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.6%; Score 332.5;
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Name=0J1191 G08.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Q6ZHP9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Petromyzontiformes; Petromyzontidae; Petromyzon.
NCBI_TaxID=7757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Acariformes; Sarcoptiformes; Astigmata; Glycyphagoidea;
Echimyopodidae; Blomia.
NCBI_TaxID=40697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Typhlosole;
MEDLINE=22971689; PubMed=14507309;
Ulinnk-001 T.S., Takezaki N., Kuroda N., Figueroa F., Sato A., Samonte I.E., Mayer W.E., Klein J.;
Phylogeny of antigen-processing enzymes: cathepsins of a cephalochordate, an agnathan and a bony fish.";
Scand. J. Immunol. 58:436-448(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; Pept cys_acsite.
Pfam; PF00112; Peptidase_C1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 31.7%; Score 382; DB 2; Length 221; 1 Similarity 38.4%; Pred. No. 3.7e-26; 86; Conservative 35; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 IVGYSNAQGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYP 217
                                                                                                                                                                                                                                                                                                                                                                                  Mora C.I., Diaz A.M., Montealegre F., Flores I.,
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF277840; AAKS8415.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cysteine protease.
272B45E5A53F2900 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                       Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0705; PAPAIN. SMART; SM00645; Pept C1; 1.
PROSITE; PS00139; THIOL_PROTEASE CYS; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <1 221 C
                                                                       Cysteine protease (Fragment).
Blomia tropicalis (Mite).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 10-MAR-2004 (TrEMBLrel. 26, 10-MBLrel. 2
01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P53634; 1K3B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Typhlosole
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
O75XQ7
AC Q75XQ
DT Q1-OC
DT 01-MC
DE Cathe
OS Butar
OX NCEL
RN (1)
RR SEQUE
RX TISSU
RR SEQUE
RX SEQUE
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Local Similarity
hes 71; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                        -QHGCHGDTIPRGIEYIQHN-GVVQESYYRYVAREQSCR--RPNAQRFGISNYCQIYPPN 123
                                                                                                                                                                                                                                                                         124 ANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQGV 183
                                                                                                                                                                                                                      202 FNHGCRGGLMDFAFAYIMGNQCIYTEEDYPYLMEEGYCREKQPHSKVITITGYEDVPANS 261
                                                                                                                                                                                                                                                                                                                    262 ETSLLKALAHQPVSVGIAAGSRD---FQFYKG-GIFDGECGIQPD-HALTAVGYGSYYGQ 316
                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

A Yamada K., Banh J., Chan M.M., Chang C.H., Chang B., Dale J.M.,

A Deng G.M., Orderath A.D., Lee J.M., Onodera C.S., Quach H.L.,

Tang C., Tordumi M., Wu H.C., Yamamura Y., Yu G., Boweer L.,

A Tang C., Tordumi M., Wu H.C., Hayashizaki Y., Ishida J., Jones T.,

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

Kamiya A., Maranda M., Narusaka M., Nguyen M., Palm C.J.,

A Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,

Bayis R.W., Ecker J.R., Theologis A.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

-I- SIMILARITY: Belongs to peptidase family Cl.

R EMBL, AY064033; AAU36389.1; -.

R EMBL, AY064033; AAU36389.1; -.
                                                                         9 NAPAEIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDCAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawi J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; __Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; F84672; F84672.
HSSP; P53634; IK3B.
GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Town C.D., Kaul S.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Theologis A.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                DYWIVRNSWDTNWGDNGY-----GYFAANIDLMMIEEYP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
35.7%; Pred. No. 1.9e-21; ive 34; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cysteine proteinase.
Name-At2g27420;
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 05-JUL-2004 (TrEMBLrel. 27,
                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                        68
                                                                                                                                                                                                                                                                                                                                                                       184
                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 CQIYPPNANKIREALAQTHSAIAVIIGIKDLD-AFRHYDGRTIIQRDNGY--QPNYHAVN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 -ETVPMNN---EEALLQAVSQQPVSVGIEGTGAAFRHYSGGVF----NGECGTDLHHAVT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CASQH--GCHGDTIPRGIEY-IQHNGVVQESYYRYVAREQSCRRPNA-----QRFGISNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 SINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQELVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 IVGYGMSEEGTKYWVVKNSWGETWGENGYMRIKRDVDAPQGMCGLAILAFYP 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Callosobruchus maculatus (cowpea weevil).
Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomelidae; Bruchinae; Bruchini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVGYS-NAQGVDYWIVRNSWDTNWGDNGYGYFAANID-----LMMIEEYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P43235; 1AYU.

GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.

GO; GO:0006508; F:cysteine-type endopeptidase activity; IEA.

InterPro; IPR000169; Peptidase_C1.

InterPro; IPR000169; Peptidase_C1.

Pfam; PF00112; Peptidase_C1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.4%; Score 331; DB 2; Length 326; 32.7%; Pred. No. 2.2e-21; Live 38; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                         27.5%; Score 332; DB 2; Length 348; 36.2%; Pred. No. 1.9e-21; ive 32; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Zhu-Salzman K., Ahn J.-E., Koiwa H., Salzman R.A.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family Cl.
EMBL; AFS44838; AAQ11969:1; --
                                                                                                        PRINTS; PROOFS; PAPAIN.

PRODON; PROOFS; PAPAIN.

SMART; SMOO645; Peptidase_Cl; 1.

PROSITE; PSOO640; THIOL PROTEASE_CNS; 1.

PROSITE; PSOO639; THIOL PROTEASE_CNS; 1.

PROSITE; PSOO639; THIOL PROTEASE_CNS; 1.

Hydrolase; Protease; Thiol protease.

SEQUENCE 348 AA; 38738 MW; EB86ABEC2B553E76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SMO0645; Pept_C1; 1.—
PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
Hydrolase; Protease; Thiol protease.
SEQUENCE 326 AA; 36653 MW; A9265E018FFD2A8D CRC64;
GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative gut cathepsin L-like cysteine protease. Name-CPA15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 AA.
                   InterPro; IPR000668; Peptidase C1.
InterPro; IPR000169; Pept cys acsite.
Pfam; PF00112; Peptidase_C1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00705; PAPAIN.—
ProDom; PD000158; Peptidase_Cl; 1.
SMART; SM00645; Pept_Cl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 36.2% nes 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Cuiliano D.B., Hong X., McKerrow J.H., Blaxter M.L., Oksov Y., Liu J., Chedin E., Lustigman S.; Cathepalan B.; Catheran B.; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 IREALAQTHSAIAVIIGIKDLDAFRHY-DGRTIIQRDNGYQPNYHAVNIVGYSNAQGV-D 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 ALAQTHSAIAVIIGIKDLDAFRHYDGRTIIOR---DNGYQPNYHAVNIVGYSNAQGVDYW 186
                                                                                                                                                                       70 GCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIYPPNANKIRE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 PAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQELVDCA---S 67
14 IDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQELVDCASQ----H 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
NCBI_TaxID=6279;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Cathepsin L-like cysteine proteinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 IVKNSWGADWGEKGYFRLKKDVKACGIGYYNPYPILL 326
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Best Local Similarity 37.99
Matches 77; Conservative
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Search completed: May 19, 2005, 17:22:44 Job time : 62 secs

protein search, using sw model OM protein - May 19, 2005, 17:12:26 ; Search time 164 Seconds (without alignments) 523.541 Million cell updates/sec Run on:

US-09-867-159A-2 1206 Title: Perfect score:

1 TNACSINGNAPAEIDLRQMR.....YFAANIDLMMIEEYPYVVIL 222 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seq seq 08 08 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aao20568 Cysteine	Abb98533 Cysteine	Aar22433 Der p I a	Aar39359 Dermatoph	Aar51727 Der p I.	Aar47063 Protein a	Aar66545 Der p I a		Aay50356 Dermatoph	Aau18959 House dus	Abg71812 European	Aar49920 Protein a	Aau07748 House dus	Aab98347 D. pteron	Aab98346 D. pteron	Aam50623 Recombina	Adk52158 Full leng	Adm57302 Modular a	Aau07746 House dus	Abg67023 House dus	Adk52140 Der pl al	Adr87225 Dust mite	Aab98345 D. pteron	Aab98331 D. pteron	Ad127398 Polypepti
3 ID	. AAO20568	3 ABB98533	: AAR22433	: AAR39359	: AAR51727	: AAR47063	PAR66545	: AAW71908	2 AAY50356	4 AAU18959	5 ABG71812	2 AAR49920	1 AAU07748	L AAB98347	AAB98346	5 AAM50623	3 ADK52158	B ADM57302	4 AAU07746	5 ABG67023	1 ADK52140	9 ADR87225	I AAB98345	4 AAB98331	3 ADL27398
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Aab98348 D. pteron Aab98330 D. pteron Aaa56747 Dermatoph Adr97692 European Aab9834 D. pteron Aay085580 D. pteron Aay0852 D. pteron Aab9832 D. pteron Aab98128 D. pteron Abb80128 Der pleron Abb80128 Der pleron Adb80128 Der pleron Adb80128 Buropean Adm57314 Modular a Adg14389 European Adm57314 Modular a Adg14389 European Ads52096 Major mit Ads1437 Der mit Ads1447 Der mit	
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ALIGNMENTS

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Antiallergic; antiinflammatory; antiasthmatic; dermatological; allergen; anti-histamine; histamine synthesis inhibitor; allergic hypersensitivity; allergic asthma; allergic rhinitis; cysteine protease protein; enzyme; atopical eczema.
AA020568 standard; protein; 222 AA.
                                                                                   Dermatophagoides pteronyssinus.
                          (first entry)
                                       Cysteine protease protein.
                          02-JAN-2003
             AA020568;
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ney Misc-difference 105

/note= "Encoded by ACC"

WO200278736-A2

10-OCT-2002

28-MAR-2002; 2002WO-FR001098.

30-MAR-2001; 2001FR-00004370. 03-MAY-2001; 2001FR-0005929. 29-MAY-2001; 2001US-00867159.

(ANTI-) ANTIALIS SARL

Trehin Y; Terrasse G, Loria E,

WPI; 2002-750636/81. N-PSDB; AAL41281. Antiallergic compositions containing an anti-histamine, a histamine synthesis inhibitor, and optionally an allergen or nucleic acid coding for the allergen.

Claim 13; Page 30-31; 32pp; French.

The invention relates to antiallergic compositions containing an anti-histemaine, a histemaine synthesis inhibitor, and optionally an allergen or isolated nucleic acid molecule that has at least one polynucleotide sequence coding for the allergen, together with a pharmaceutical carrier.

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27-AUG-2003
04-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                       ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
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                                                                                                                                                                                                                                                                           Gaps
The pharmaceutical composition of the invention is useful as a nonspecific antiallergic treatment, and also useful in the treatment of allergic hypersensitivity, allergic asthma, allergic rhinitis, and allergic and atopical eczema. This sequence represents the cysteine protease protein relating to the antiallergic compositions of the
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                                                                                                                                                                                                                        Length 222;
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N-PSDB; ABQ80833.
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The present invention relates to an antiallergic pharmaceutical

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composition (1) comprising a pharmaceutical carrier containing an active agent combination of at least two of: an allergen; an antihistenanine; and a histemaine synthesis inhibitor. (1) is used for treating or preventing allergic hypersensitivity reactions, especially allergic asthma, allergic thintis or allergic atopic eczema, in babies, children or adults. The present sequence is cysteine protesse from Dermatophagoides pteronivssinus, which was used as an allergen in the invention
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                                                                                                                                                                                                                                                                                                                   120
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100.0%; Pred. No. 2.7e-127;
ive 0; Mismatches 0;
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/note= "Bignal peptide cleavage"
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                                                                                                                                         Sequence 222 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was obtd. in plasmid form as subclone from lambda gtil (Chua et al., J. Exp. Med. 167: 175-182 (1988)). The CDNA was used to express a Dep pl allergen which was capable of raising an immune response when contacted with anti-Dep pl antibodies. The protein was used to design a series of overlapping peptides synthesised by standard techniques to cover the whole Dermatophagoides pteronyssinus Dep pl sequence. The T cell epitopes
                                                                                                                                                                                                                                                            ELVDCASQHGCHGDT1PRGIEY1QHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                                          143
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                                                                                                                                                                                                                                                                                                                                       PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 203
The protein sequence was deduced from the cDNA sequence obtd. by screening a dermatophagoides cDNA library with two probes comprising the Der p 1 cDNA Bamil fragments 1-348 and 349-857. The protein allergen is used as a diagnostic reagent in detecting and treating sensitivity to house dust mites and in desensitisation therapy. See also AAR22431,2. (Updated on 27-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                   ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY
                                                                                                                                                                                                TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
                                                                                                                                                                       Gaps
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                                                                                                                                      Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house dust mite; allergy; soluble; allergen
                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                  QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                      100.0%; Score 1206; DB 2; 100.0%; Pred. No. 3.1e-127;
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                                                                                                                                                                     Mismatches
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92US-00881396.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                   222; Conservative
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                                                                                                                                                       Local Similarity
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                                                                                                         Sequence 245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell epitope;
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12-AUG-1993
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of the protein were mapped by detection of the peptide's ability to stimulate T cell activity. The peptides may be used for diagnosis and treatment of sensitivity to house dust mite allergens. When administered to house dust mite sensitive individuals, the peptides are capable of modifying the allergic response to the allergens. The peptides may be modified for e.g. increasing solubility, enhancing therapeutic or preventive efficacy or stability. See also ARR34686-700, AAR36398-490 and AAR39360-2. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                       PDNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated and/or modified peptides comprising T-cell epitopes - of major protein allergens of genus Dermatophagoides, used to treat or diagnose sensitivity to house dust mites.
                                                                                                                                                                                                                                                                                                                                         ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY
                                                                                                                                                                                                                                                                                   TNACSINGNAPABIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEO
                                                                                                                                                                                                                                                                                                                                                                                     PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA
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                                                                                                                                                                                                                                                                                                                    ELVDCASOHGCHGDT1PRG1EY1OHNGVVQESYYRYVAREQSCRRPNAQRFG1SNYCQ1Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1206; DB 2;
100.0%; Pred. No. 3.1e-127;
ive 0; Mismatches 0;
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                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 222; Conservative
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N-PSDB; AAQ62308
                                                                                                                                                    Sequence 245 AA;
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This sequence represents the group I protein allergen from the house dust mite D. pteronyssinus, Der pi. The Der pi protein shows high homology co to the group I protein allergen derived from D. farinae, Der fi, having an identity of 81%. Fragments of these proteins, and the corresponding group II allergens, Der pi II and Der fii, (see AAR51731-841) represent comparises. The protein peptides may be produced which comprise at least two or these antigenic fragments. Each region of these petides may be charited from the same, or different, mite allergens. The antigenic fragments may be produced by chemical synthesis, chemical cleavage of the protien allergen or by recombinant techniques. These peptides may be produced by chemical synthesis, chemical cleavage of the protien allergen or by recombinant techniques. These peptides may be produced by chemical synthesis, chadividual, are capable of modifying the allergic response of the individual to the allergen. These peptides do not bind to immuno-globulin E [IgE), or bind IgE to a lesser extent than the full length protein allergen. This reduces the major complications of standard immunotherapy, which are IgE-mediated responses such as anaphylaxis. Exposure of mite allergens such that they become unresponsive to mite callergens and do not participate in mounting an immune response upon exposure. Administration of the peptide may also modify the lymphokine content profile as compared with exposure to the naturally occuring mite and an and an and the peptide may also modify the lymphokine contents.
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/label= cleavage site
/note= "cleavage between pro-Der pI and pre-Der
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1206; DB 2; Length 245; 100.0%; Pred. No. 3.1e-127;
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/label= Der pI preproenzyme
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/label= Cleavage site
/note= "proenzyme remains"
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les 222; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 245 AA;
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17-OCT-1994
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AAR47063 is a preproenzyme Der pI. The amino acid sequence preceding the mature protein sequence contains cleavage sites for the pre- and procenzyme forms, with residues 1-11 corresponding to a partial signal peptide sequence. The mature protein can be used to detect sensitivity in an individual to house dust mitte and to reduce the sensitivity of the individual. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 245;
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100.0%; Pred. No. 3.1e-127;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR66545 standard; protein; 245 AA.
                                                                                                                                                                                                                                                    Example 1, Fig 1, 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dermatophagoides pteronyssinus
                                         93WO-US008518
                                                                       92US-00945288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-00072832
                                                                                                    (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-AU000292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 222, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                            WPI; 1994-101195/12.
N-PSDB; AAQ58665.
                                                                                                                                 Thomas WR, Chua K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Der p I allergen.
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cryptic epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUN-1993;
                                         10-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9427634-A1
                                                                       10-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
31-JUL-1995
             17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR66545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR66545
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93WO-US003471.
94US-00227772.
95US-00445307.
                                                                           Evans S,
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                                                  (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                         , Kuo M,
Rogers BL;
                                                                                                              WPI; 1998-567590/48.
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dermatophagoides
                                                                                                                           N-PSDB; AAV61384
                                                                                                                                                                                                                                                                                                                                                         Sequence 245 AA;
14-APR-1993;
14-APR-1994;
19-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2000
                                                                           Franzen HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5968526-A
                                                                                                                                                                                                                                                                                                                                                                                                          Matches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-OCT-1999
                                                                                       Shaked Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY50356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                  allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY50356
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                           a compan. Contig. at least one cryptic peptide derived from that antigen. BIO mice were immunised with various Der p I peptides and then response to Der p I and the peptides was measured in the presence of spleen adherent cells. Peptides contg. amino acids 120-143 and 144-169 of Der p I were positive i.e., they contained cryptic epitopes. The cDNA fragment encoding amino acids 131-187 of Der p I was cloned into pGEX and expressed in bacteria as a fusion protein with glutathione-S-transferase. Mice were given orally 3 mg of this protein on 3 consecutive days, then 7 days later immunised subcutaneously with native Der p I in complete Freund's adjuvant. Seven days later lymph nodes, stimulated with protein or synthetic peptides, were assayed for lymphokines (IL-2). Mice given the cryptic epitope had a much weaker response than those treated only with buffer. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPNANKIREALAQTHSAIAVIIGIKDLAPRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 203
                                                                                     immunological tolerance with cryptic peptide - esp from allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                      TNACSINGNAPAEIDLROMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p I,
                                                                                                                                                   Immunological tolerance to a protein antigen may be induced by admin. of
                                                                                                                                                                                                                                                                                                                                                                                                                    1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genus Dermatophagoides; major protein allergen; T cell epitope; Der Der p II; Der f I; Der f II; house dust mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                    Length 245;
                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 245
                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1206; DB 2; 100.0%; Pred. No. 3.1e-127;
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                          Disclosure; Page 22-23; 38pp; English.
                                                                                                auto:antigen, esp admin orally.
                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW71908 standard; protein; 245
(CHIL-) INST CHILD HEALTH RES
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                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dermatophagoides Der p I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                               WPI; 1995-022467/03.
N-PSDB; AAQ79618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dermatophagoides.
                                                                                                                                                                                                                                                                                                                                            Sequence 245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-2003
25-MAR-2003
16-DEC-1998
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                         Thomas WR;
                                                                                   Inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                               24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW71908;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
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AAW71908
임
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The present invention describes peptides for treating sensitivity to house dust mite allargens from the genus Dermatophagoides. Peptides within the scope of the invention comprise at least one T cell epitope, or preferably at least two T cell epitopes of a protein allergen selected from the allargens Der p I, Der p II, Der f I, or Der f II. The invention also describes modified peptides having similar or enhanced therapeutic properties as the corresponding, naturally occurring allargen, but having reduced side effects. The present sequence represents Der p I from the present invention. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 27-AUG-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                     Dermatophagoides allergen peptides – useful for treating house dust mite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Allergen; house dust mite; detection; sensitivity; T cell epitope; screening; allergic disorder; asthma; rhinitis; ectopic dermatitis; Der p I.
Chen X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 245;
Greenstein JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIBEYPYVVIL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dermatophagoides sp. allergen Der p I protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1206; DB 2; 100.0%; Pred. No. 3.1e-127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
Garman RD,
                                                                                                                                                                                                                                                                                                   Col 69-72; 155pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ź
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Chen X;

Franzen HM,

Garman

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The invention relates to an isolated peptide of the major protein allargens of the genus Dermatophagoides, which comprises at least one T cell group of a protein allargen from Der (DP) I, DP II, Der f (DF) I or DF II. The isolated peptide comprises at least two regions, each region comprising at least one T cell group of a protein allargen of the genus Dermatophagoides. The regions are derived from the same or different protein allargens of the genus Dermatophagoides. The peptides are useful for treating house dust mite allargy in humans. The peptides are also useful for detecting or diagnosing sensitivity to house dust mite protein allargems. The present peptides have similar or enhanced therapeutic properties as the naturally-occurring allargen, but have reduced side effects, and increased solubility and stability. The present sequence represents an allargenic protein from Dermatophagoides from which the T-cell epitope containing peptides are derived
                                                                                                                                                                                                                                                                                                                                                                                                                        Peptides comprising T cell groups of the major allergens from
Dermatophagoides (house dust mites), useful for treating house dust mite
allergy in humans, and for diagnosing sensitivity to house dust mite
                                                                                                                                                                                                                                                                                        Rogers BL,
                                                                                                                                                                                                                                                                                          Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG71812 standard; protein; 245
                                                                                                          91US-00777859.
92US-00881396.
93WO-US003471.
                                                                                                                                                                           94US-00227772.
                                                                   95US-00484296
                                                                                                                                                                                                                                              (IMMU-) IMMULOGIC PHARM CORP.
                                                                                                                                                                                                                                                                                          Greenstein JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                         2001-549074/61
                                                                                                                                                                                                                                                                                                             Shaked Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        allergy in humans
protein allergens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 245 AA;
                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS30721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JAN-2003
                                                                07-JUN-1995;
                                                                                                            16-OCT-1991;
                                                                                                                                                                                4-APR-1994;
                                                                                                                                                                                                  19-MAY-1995;
                       31-JUL-2001
                                                                                                                                                         14-APR-1993
                                                                                                                                    18-MAY-1992
                                                                                                                                                                                                                                                                                             Garman RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                  Evans S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel method (1) for detecting whether an individual is sensitive to Dermatophagoides (house dust mites). The method involves detecting sensitivity to house dust mites in patients, comprising combining a blood sample from the individual with 1 or more isolated T cell epitopes of the protein allergens I and II (IPP I) and (IP II)) from Dermatophagoides (house dust mites). 32 T cell epitopes with varying, defined amino acids sequences (given in the specification) may be used in (I). The sample and allergens are combined under conditions appropriate for the binding of blood components with the polypeptides. The extent of binding is then indicative of the sensitivity of the patient to house dust mites. (I) may be used to screen individuals for sensitivity to Dermatophagoides (house dust mites). The house dust mite is a major cause of a variety of allergic disorders such as asthma, rhintis and eccopic dermatitis. This sequence represents the house dust
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELVDCASQHGCHGDTIPRGIEY1QHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                   Screening individuals for allergic reactions to T cell epitopes of major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 TNACSINGNAPAEIDLRQMRTVTPIRMQGGGGSCWAFSGVAATESAYLAHRNQSLDLAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dust mite, allergenic protein, Der p I; Der f I; II; antiallergenic; immunostimulant; house dust mite allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                    Shaked Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1206; DB 2; Length 245; 100.0%; Pred. No. 3.1e-127; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                    Franzen HM,
                                                                                                                                 Greenstein JL, Rogers BL, ans S, Kuo M;
                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 73-74; 158pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU18959 standard; protein; 245 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        House dust mite allergen Der p I.
                                                                                                                                                                                                                                                                                          allergens from house dust mites.
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    94US-00227772
                       95WO-US004481
95US-00445307
                                                                                        (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 222; Conservative
                                                                                                                                                         Evans S, Kuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mite allergen Der p I
                                                                                                                                                                                                  WPI; 1999-590385/50.
N-PSDB; AAZ23906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T-cell epitope
14-APR-1994;
12-APR-1995;
19-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-2001
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                                                                                                                                                                                                                                                                   61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                                                                                             PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                                                                                                                                   84 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 143
The present
                                                                                                                                                                                        9
                                                                                                                                                                                                                           83
                                                                                                                                                                                                         24 TNACSINGNAPAEIDLRQMRTYTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ
                                                                                                                                                                                        1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
                                                                                                                                                    Gaps
                                                                                                                                                  0
                                                                                                               Length 245;
                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              204 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLWMIEEYPYVVIL 245
                                                                                                                                                                                                                                                                                                                                                                                                                            OGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                           100.0%; Score 1206; DB 4;
100.0%; Pred. No. 3.1e-127;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European house dust mite Der p I protein.
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US6268491-B1

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The present invention relates to a new DNA encoding a peptide from Dermatophagoides farinae protein allergen, designated Der f I or Der f II, that comprises at least one epitope of the protein allergen. The invention is useful for producing a peptide from Der f I or Der f II, that comprises at least one epitope of the protein allergen. The invention is also useful for diagnosing, treating protein allergen. The invention is also useful for diagnosing, treating cand preventing allergic responses to mite allergens, particularly, the mites D. farinae. The invention is also useful for diagnosing treating additional nucleotide sequences coding for mite allergens having amino acid sequences similar to Der f II. The peptide is useful for detecting sensitivity in an individual to house dust mites and can be used to treat sensitivity (reduce sensitivity or desensitise) in an individual, to whom therapeutically effective quantities of D. farinae peptide is administered. The peptides when administered to sensitive individual modify the individual's allergic response to Der f I or Der f II. The peptides are also useful as purified allergens useful in the standardisation of allergen extracts or preparations which can be used as reagents for diagnosis and treatment of allergy to house dust mites. The epitopic peptides are useful as diagnostic reagents for determining reactivity to the mite species. The peptides are also useful for determining reactivity to the mite species and/or B cell epitopes and/or B rell epitopes which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                Dermatophagoides farinae protein allergen; Der f I; ber f II; allergy; allergic response; mite allergen; house dust mite; T cell epitope; B cell epitope; antiallergic; desensitisation therap; modifies allergic response of house dust mite-sensitive individual; modifiy B-cell and/or T-cell response to Der f I and Der f II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated DNA encoding peptide from Dermatophagoides farinae p. allergen, designated Der f I and Der f II, useful for treating and preventing allergic responses to mite allergens, by desensitization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 7; 22pp; English.
                                                                                                         modify B-cell and/or T-cell resp
European house dust mite; Der p
                                                                                                                                                                          Dermatophagoides pteronyssinus.
                                                                                                                                                                                                                                                                                                                                                                       90US-00580655.
93US-00107332.
93US-00175071.
                                                                                                                                                                                                                                                                                                         99US-00295188
                                                                                                                                                                                                                                                                                                                                                    90US-00458642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMMU-) IMMULOGIC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-672946/72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chua K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABS56342
                                                                                                                                                                                                                                                                                                                                                                         11-SEP-1990;
16-AUG-1993;
29-DEC-1993;
                                                                                                                                                                                                                   US6423837-B1
                                                                                                                                                                                                                                                                                                         20-APR-1999;
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ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                 Score 1206; DB 2;
Pred. No. 4.6e-127;
; Mismatches 0;
Example 1; Fig 21; 98pp; English.
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                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                    Similarity
                                                                                                                                                                 Sequence 320 AA;
                                                                                                                                                                                                                                     222;
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                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                     ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                             TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 83
                                                      occur.
                              of importance in allergic responses to D. farinae allergens and to elucidate the mediators or mechanisms of by which these reactions occur. The present amino acid sequence represents the Buropean house dust mite Der p I protein as described in the invention
                                                                                                                                                                                                                                       TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                     ö
                                                                                                                                                               Length 245;
                                                                                                                                                                                                   Indels
                                                                                                                                                               100.0%; Score 1206; DB 5;
100.0%; Pred. No. 3.1e-127;
ive 0; Mismatches 0;
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                  Local Similarity
nes 222; Conserv
                                                                                                                              Sequence 245 AA;
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                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                    Query Match
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AAR49920 is a preproenzyme Der pl. The amino acid sequence preceding the mature protein sequence contains cleavage sites for the pre- and proenzyme forms, with residues 1-97 corresponding to a partial signal peptide sequence. The mature protein can be used to detect sensitivity in an individual to house dust mite and to reduce the sensitivity of the individual. (Updated on 25-MAR-2003 to correct PN field.)
144 PPNANKIREALAQTHSALAVIIGIKOLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNACSINGNAPAEIDLROMRTVTPIRMOGGCGSCWAPSGVAATESAYLAHRNOSLDLAEO 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNACSINGNAPABIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New protein allergens of house dust mite - used for diagnosing and treating sensitivity in an individual to house dust mite allergens
                                                                                                                                                                                                                                                                                                                                                                                                 pre-Der
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                   /label= cleavage site
/note= "cleavage between pro-Der pl and
                                                 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                                                                                                                                                                                           .. .322
|abel= Der pI preproenzyme
                                                                                                                                                                                                                                                                                                                                   83. .85
/label= Cleavage site
/note= "proenzyme remains"
85. .97
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                           Der pI; House Dust Mite Allergen.
                                                                                                                           AAR49920 standard; protein; 320
                                                                                                                                                                                                                                                                    Dermatophagoides pteronyssinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93WO-US008518.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92US-00945288
                                                                                                                                                                                                                Protein allergen of Der pl.
                                                                                                                                                                                         (first entry)
                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-101195/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chua K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ58669
                                                                                                                                                                                                                                                                                                                                    Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                          Cleavage-site
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                                                                                                                                                                            25-MAR-2003
                                                                                                                                                                                           17-0CT-1994
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                                     181
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                                                                                                                                                    AAR49920;
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                                                                                                    RESULT 12
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The invention relates to an isolated peptide of the major protein alergens of the genus Dermatophagoides, which comprises at least one T cell group of a protein allergen from Der p (DP) I. Der f (DP) I or DF II. The isolated peptide comprises at least two regions, each region comprising at least one T cell group of a protein allergen of the genus Dermatophagoides. The regions are derived from the same or different protein allergens of the genus Dermatophagoides. The peptides are useful for treating house dust mite allergy in humans. The peptides are useful for detecting or diagnosing sensitivity to house dust mite protein allergens. The present peptides have similar or enhanced therapeutic properties as the naturally-occurring allergen, but have reduced side effects, and increased solubility and stability. The present equence represents an allergenic protein from Dermatophagoides from which the T-cell epitope containing peptides are derived, a polymorphic variant of Der p I. Note: The present sequence is not shown in the
PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides comprising T cell groups of the major allergens from Dermatophagoides (house dust mites), useful for treating house dust mite allergy in humans, and for diagnosing sensitivity to house dust mite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen X;
                                                                                                                                                                                                                                                                                                                                                              House dust mite; allergenic protein; Der p I; Der p II; Der f I; Der f II; antiallergenic; immunostimulant; house dust mite allergy; T-cell epitope; polymorphic variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rogers BL, Franzen HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild-type Ser substituted by Thr"
                                                                                                                                    QGVDYWIVRNSWDTNWGDNGYGYFAANIDLAMIEEYPYVVIL 320
                                                                                                                 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                                                                                                                                                                                                              House dust mite allergenic protein Der p I variant d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                               AAU07748 standard; protein; 222 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                Dermatophagoides pteronyssinus.
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92US-00881396.
93WO-US003471.
94US-00227772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Greenstein JL,
                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein allergens.
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                                                                                                                                                                                                                                                                                               04-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-2001
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                                                                                 219
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                                                                                                                                                                                                                                                                                              121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                       61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for the production of a recombinant mite Group 1 protein (1). The method comprises culturing a methyltrophic yeast microorganism transformed with a nucleic acid molecule (II) encoding (I), and recovering (I), or culturing Escherichia inclusion body in E. coli, isolating the inclusion body, and recovering (I). Also described is a method for detecting mite allergy in an animal comprising: (a) contacting (I) with a putative IgE-containing substance of form a complex between (I) and IgE, and (b) determining the presence of IgE reactive with (I) by detecting the complex, where the presence of reactive IgE is indicative of mite allergy in the animal (I) is useful
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specification but is derived from the Der p I sequence shown in figure
                                                                                                                                                                           1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
                                                                                                                                              1 TNACSINGNAPAEIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mite group 1 protein; methyltrophic yeast; Escherichia coli; allergy; recombinant mite group 1 protein; allergic response; antiallergic; infectious disease; allergic disease.
                                                                                                             Gaps
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                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                          181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLAMIEEYPYVVIL 222
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                                                                     Score 1203; DB 4;
Pred. No. 5.8e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D. pteronyssinus Der p 1 protein SEQ ID NO:82.
                                                                                                         1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB98347 standard; protein; 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dermatophagoides pteronyssinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0159841P.
                                                                     tch 99.8%;
al Similarity 99.5%;
221; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAH22385
                                    Sequence 222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200129078-A2
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                                                                       Query Match
Best Local &
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                                                                                                                                                                                                                                                                             ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method for the production of a recombinant mite Group 1 protein (I). The method comprises culturing a methyltrophic yeast microorganism transformed with a nucleic acid molecule (II) encoding (I), and recovering (I), or culturing Escherichia coli transformed with (II) under conditions in which (I) forms an inclusion body in E. coli, isolating the inclusion body, and recovering
                                                                                                                                                                                                                                           9
for detecting mite allergy in an animal, or in a composition to reduce allergic response to a mite Group 1 protein in a mite allergic animal. (1) is also useful in a composition for treating or preventing allergic, infectious or other diseases. AAH22326 to AAH22394 and AAB89326 to AAB98349 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing recombinant mite Group 1 protein for treating allergies, involves culturing a methyltrophic yeast microorganism or Escherichia coli transformed with nucleic acid molecule, and recovering the protein.
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                                                                                                                                              Length 222;
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Pred. No. 1.3e-126;
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                                                                                                                                                                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB98346 standard; protein; 302
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                                                                                                               Sequence 222 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising: (a) contacting (I) with a putative IgB-containing substance to form a complex between (I) and IgB; and (b) determining the presence of IgB reactive with (I) by detecting the complex, where the presence of reactive IgB is indicative of mite allergy in the animal. (I) is useful for detecting mite allergy in an animal, or in a composition to reduce allergy in an animal, or in a composition to reduce allergy in an animal, or in a composition to reduce allergic response to a mite Group 1 protein in a mite allergic animal. (I) is also useful in a composition for treating or preventing allergic, infectious or other diseases. AAH22326 to AAH22394 and AAB98326 to AAB98349 represent sequences used in the exemplification of the present
(I). Also described is a method for detecting mite allergy in an animal
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Matches 221;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                          1434725 segs, 334507595 residues
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1206
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Searched:

Published Applications AA:*

1: /cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
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19: /cgn2_6/prodata/2/pubpaa/USO0_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

;	Appli	Appl	ppli	Appl	179, App	Appli	Appl	Appl	Appl	Appl	Appl	Appl	41, Appl
	7	88	Α.	79,	179	8,	32,	11,	20,	35,	38,	14,	41,
Description	Sequence	Sequence 88, App]	Sequence 2, Appli	Sequence 79, Appl	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 35,	Seguence	Seguence	Seguence
QI	US-09-867-159A-2	US-10-001-245-88	US-09-877-160-2	US-09-847-208-79	US-10-001-245-179	US-10-892-543-8	US-10-892-543-32	US-10-892-543-11	US-10-892-543-20	US-10-892-543-35	US-10-892-543-38	US-10-892-543-14	US-10-892-543-41
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Sequence 26, Appl	Sequence 18, Appl	20,	Sequence 24, Appl	5,7	7	22,	٦	16,	23,	.17,	29,	56	30	28	34	32	18	Sequence 181, App	Sequence 180, App	73	18	95	184,	Sequence 185, App	1354	_	48978		Sequence 43777, A	Sequence 2, Appli	Sequence 2, Appli
US-10-001-245-26	US-10-001-245-18	US-10-001-245-20	US-10-001-245-24	US-10-892-543-5	US-10-892-543-2	US-10-001-245-22	US-10-001-245-14	US-10-001-245-16	US-10-892-543-23	US-10-892-543-17	US-10-892-543-29	US-10-892-543-26	US-10-001-245-30	US-10-001-245-28	US-10-001-245-34	US-10-001-245-32	US-10-001-245-182	US-10-001-245-181	US-10-001-245-180	US-09-847-208-73	US-10-001-245-183	US-09-847-208-95	US-10-001-245-184	US-10-001-245-185	-13	US-10-259-165-184	US-10-425-114-48978	14	US-10-425-114-43777	US-09-953-956-2	US-10-114-464-2
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96.4	96.3	96.3	96.3	96.2	96.2	96.1	95.9	95.9	95.9	95.4	95.0	95.0	94.8	94.7	93.9	93.9	86.3	86.0	86.0	82.7	82.7	81.5	81.5	78.3	27.6	27.6	27.4	26.9	26.9	26.8	26.8
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ALIGNMENTS

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APPLICANT: ANTIALIS

TITLE OF INVENTION: Anti-allergic pharmaceutical composition containing at least one TITLE OF INVENTION: Anti-allergic pharmaceutical composition containing at least one FILE OF INVENTION: and at least one anti-histamine compound FILE OF INVENTION: and at least one anti-histamine compound CURRENT PROPERTY OF UNMERS: US/09/867,159A

CURRENT FILING DATE: 2001-05-29

PRIOR APPLICATION NUMBER: FR01/04370

PRIOR APPLICATION NUMBER: FR01/04370

PRIOR APPLICATION NUMBER: FR01/05929

PRIOR APPLICATION NUMBER: FR01/05-03

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1

SEQ ID NO 2

LENGTH: 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Dermatophagoides pteronyssinus
                   Sequence 2, Application US/09867159A Publication No. US20030104013A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 222; Conservative
JS-09-867-159A-2
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                                                                                                                        Query Match 99.2%; Score 1196; DB 9; Best Local Similarity 99.1%; Pred. No. 2.3e-117; Matches 220; Conservative 1; Mismatches 1;
                        TYPE: PRT ; ORGANISM: Dermatophagoides pteronyssinus US-09-877-160-2
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                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: IPSEN, JOSGEN N. APPLICANT: IPSEN, JOSGEN N. APPLICANT: LARSEN, JOSGEN N. APPLICANT: LARSEN, JOSGEN N. APPLICANT: LARSEN, JOSGEN N. APPLICANT: SPANGFORT, Michael D. TITLE OF INVENTION: NO. US20030175312Alel mutant allergens FILE REFERENCE: 4305/11942-US2 CURRENT APPLICATION NUMBER: US 105/1001,245 CURRENT PILLING DATE: 2001-01-11-15 PRIOR APPLICATION NUMBER: US 60/299,361 PRIOR APPLICATION NUMBER: US 60/299,361 PRIOR APPLICATION NUMBER: US 60/299,361 PRIOR FILING DATE: 2000-11-16 NUMBER OF SEQ ID NOS: 217 SOFTWARE: PALENTIN VERBION 3.1
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Publication No. US20020197268A1

GENERAL INFORMATION:

APPLICANT: Ching-Healing, Heu

TITLE OF INVENTION: ALLERGEN-CONTAINING MILK FOR ALLERGY

TITLE OF INVENTION: TREATMENT;

FILE REFERENCE: 12774-003001

CURRENT APPLICATION NUMBER: US/09/877,160

CURRENT FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 10

SOFTWARE FEACE FOR Windows Version 4.0
                                                                                                                                                                                                QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
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US-10-001-245-88
                                                                                                                                                                                                                                                                                                                                  ; Sequence 88, Application US/10001245; Publication No. US20030175312A1; GENERAL INFORMATION:
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les 220; Conserv
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US-10-001-245-88
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US-09-877-160-2
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Sequence 79, Application US/09847208
Sequence 79, Application US/09847208
Sequence 79, Application US/09847208
Sequence 79, Application US/09011
SERENAL INFORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: Saxon, Andrew
TITLE OF INVENTION: EUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
TITLE REFERENCE: UG67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: '2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
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US-10-001-245-179
Sequence 179, Application US/10001245
Publication No. US20030175312A1
GENERAL INFORMATION:
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Sequence 11, Application US/10892543
Publication No. US20050053615A1
GENERAL INFORMATION:
APPLICANT: Best, Blaine A.
TITLE OF INVENTION: VARIANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE
TITLE OF INVENTION: DUST MITE ALLERGY
FILLE REPERENCE: AL-10
CURRENT APPLICATION NUMBER: US/10/892,543
CURRENT FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: 60/487,812
PRIOR FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Best, Elaine A.
APPLICANT: Best, Elaine A.
APPLICANT: McDermott, Martin J.
TITLE OF INVENTION: VARIANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE
TITLE OF INVENTION: DUST MITE ALLERGY
FILE REPERENCE: AL-10
CURRENT APPLICATION NUMBER: US/10/892,543
CURRENT FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: 60/487,812
PRIOR FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 42
SEQ ID NO 32
LENGTH: 303
                                                                                           201 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 260
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                   141 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Dermatophagoides preronyssinus
                                                                                                                                                                                                                                                                                                                          ; Sequence 32, Application US/10892543; Publication No. US20050053615A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              RESULT 7
US-10-892-543-32
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APPLICANT: Best, Elaine A.

APPLICANT: Best, Elaine A.

TITLE OF INVENTION: VARIANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE TITLE OF INVENTION: DUST MITE ALLERGY
FILE REFERENCE: AL-10

CURRENT PAPLICATION NUMBER: US/10/892,543

CURRENT FILING DATE: 2004-07-15

PRIOR FILING DATE: 2003-07-16

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin version 3.2

SEQ ID NO 8
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APPLICANT: HOLM, Jens
APPLICANT: IPSEN, Henrik
APPLICANT: ILASEN, Jorgen N.
APPLICANT: LARSEN, Jorgen N.
APPLICANT: LARSEN, JORGEN N.
TITLE OF INVENTION: NO. US20030175312A1e1 mutant allergens
TITLE OF INVENTION: NO. US20030175312A1e1
TITLE OF INVENTION: NO. US20030175312A1e1
CURRENT APPLICATION NUMBER: US 60/298,170
PRIOR PILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/299,361
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFFWARE: Patentin version 3.1
SEQ ID NO 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.2%; Score 1196; DB 14; Length 320; 99.1%; Pred. No. 2.3e-117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Dermatophagoides pteronyssinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.1
Matches 220; Conservative
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Matches 220;
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## Sequence 38, Application US/10892543

| Fublication No. US20050053615A1 |
| Fublication No. US20050053615A1 |
| GENERAL INFORMATION: DECEMBER |
| APPLICANT: Best, Blaine A. |
| APPLICANT: Best, Blaine A. |
| TITLE OF INVENTION: UNSTANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE |
| TITLE OF INVENTION: UNSTANT SOF MITE ALLERGY |
| FILE REFERENCE: AL-10 |
| CURRENT APPLICATION NUMBER: US/10/892,543 |
| CURRENT FILING DATE: 2003-07-15 |
| PRIOR APPLICATION NUMBER: 60/487,812 |
| PRIOR APPLICATION NUMBER: 60/487,812 |
| PRIOR APPLICATION NUMBER: 5003-07-16 |
| NUMBER OF SEQ ID NOS: 42 |
| SEQ ID NO 38 |
| LENGTH: 303
        TITLE OF INVENTION: UDST MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE TITLE OF INVENTION: DUST MITE ALLERGY
FILE REPERENCE: AL-10
CURRENT APPLICATION NUMBER: US/10/892,543
CURRENT APPLICATION NUMBER: 60/487,812
PRIOR APPLICATION NUMBER: 60/487,812
PRIOR APPLICATION NUMBER: 60/487,812
PRIOR PILING DATE: 2003-07-16
NUMBER OF SEQ 1D NOS: 42
SOFTWARE: Patentin version 3.2
SQFTWARE: Patentin version 3.2
LENGTH: 303
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97.5%; Score 1176; DB 17;
Best Local Similarity 98.2%; Pred. No. 2.8e-115;
Matches 218; Conservative 1; Mismatches 3;
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Pred. No. 2.8e-115;
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Best Local Similarity 98.2
Matches 218; Conservative
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Publication No. US20050053615A1
GENERAL INFORMATION:
APPLICANT: Best, Elaine A.
APPLICANT: Best, Elaine A.
APPLICANT: McDermoct, Martin J.
TITLE OF INVENTION: VARIANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE
TITLE OF INVENTION: DUST MITE ALLERGY
FILE REFRENCE: AL-10
CURRENT PILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: 06/487,812
PRIOR APPLICATION NUMBER: 60/487,812
PRIOR PILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.2
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                                                                             Length 302;
                                                                                                                             Indels
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                                                                     Score 1180; DB 17;
Pred. No. 1e-115;
1; Mismatches 2;
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LENGTH: 303
LYPE: PRT
ORGANISM: Dermatophagoides pteronyssinus
ORGANISM: Dermatophagoides pteronyssinus
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                                                                        Query Match
Best Local Similarity 98.6%;
Matches 219; Conservative
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Matches 218; Conservative
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US-10-892-543-20
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US-10-892-543-35
  ; ORGANISM: Del
US-10-892-543-11
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                      Indels
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96.4%; Pred. No. 5.5e-114;
tive 3; Mismatches 5;
  97.7%; Pred. No. 3.1e-114;
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APPLICANT: HOLM, Jens
APPLICANT: IPSEN, Henrik
APPLICANT: LARGEN, Jorgen N.
APPLICANT: SPANGFORT, Michael D.
APPLICANT: SPANGFORT, Michael D.
TILLE OF INVENTION: NO. UG20030175312Alel mut
FILE REFERENCE: 4305/1H942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/298,170
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ; ORGANISM: Dermatophagoides pteronyssinus US-10-001-245-26
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Best Local Similarity 96.44
Matches 214; Conservative
  Best Local Similarity 97.7
Matches 217; Conservative
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IPSEN, Henrik
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US-10-892-543-14

i Sequence 14, Application US/10892543

i Sequence 17, Etaine No. US20050053615A1

j GENERAL INFORMATION:
 APPLICANT: Best, Etaine A.

TITLE OF INVENTION: UARIANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE

TITLE OF INVENTION: DUST MITE ALLERGY

TITLE OF INVENTION: DUST MITE ALLERGY

TITLE OF INVENTION: UANBER: US/10/892,543

CURRENT APPLICATION NUMBER: US/10/892,543

CURRENT APPLICATION NUMBER: 60/487,812

PRIOR APPLICATION NUMBER: 60/487,812

PRIOR PILING DATE: 2003-07-16

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin version 3.2
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Publication No. US20050053615A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: VARIANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE
TITLE OF INVENTION: UNST MITE ALLERGY
TITLE OF INVENTION: UNST MITE ALLERGY
FILE REFREENCE: AL-10
CURRENT APPLICATION NUMBER: US/10/892,543
CURRENT FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: 60/487,812
PRIOR PLILING DATE: 2003-07-16
NUMBER OF SEQ 1D NOS: 42

SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
202 PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                           181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLAMIEEYPYVVIL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGVDYWIVRNSWDTNWGDNGYGYFAANIDLAMIEEYPYVVIL 302
                                                                  262 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.0%; Score 1170; DB 17;
98.2%; Pred. No. 1.2e-114;
tive 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Dermatophagoides pteronyssinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Dermatophagoides pteronyssinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 218; Conservative
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Best Local Similarity
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US-10-892-543-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-892-543-14
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LENGTH: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 14
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61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ELVDCASQHGCHGDTIPQGIEYIQHNGVVQESYYRYVAQEQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TNACSINGNAPAEIDLRQMETVTPIRMQGGGSCWAFSGVAATESAYLAVRNQSLDLAEQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 96.3%; Score 1161; DB 14; Length 222; Best Local Similarity 96.4%; Pred. No. 7e-114; Matches 214; Conservative 3; Mismatches 5; Indels 0.
APPLICANT: LARSEN, Jorgen N.
APPLICANT: SPANGFORT, Michael D.
TITLE REPERIOR OF US20030175312A1el mutant allergens
FILE REPERENCE: 4305/114942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/298,170
PRIOR APPLICATION NUMBER: US 60/298,170
PRIOR APPLICATION NUMBER: US 60/249,361
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 18
LENGTH: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-18
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Search completed: May 19, 2005, 17:35:46 Job time : 133 8ecs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 19, 2005, 17:21:46 ; Search time 43 Seconds (without alignments) 385.397 Million cell updates/sec

US-09-867-159A-2 1206 1 TNACSINGNAPAEIDLRQMR......YFAANIDLMMIEEYPYVVIL 222 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

513545 seqs, 74649064 residues Searched:

Total number of hits satisfying chosen parameters:

513545

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	7	7	7	Sequence 2, Appli	7	7	~	10,	10,	10,	٠.	10,	11,	11,	17	1,	1,	'n	ý	ģ	ý	ģ	ģ	Seguence 6, Appli	ģ	6,
SOUTHERNESS	ID	US-07-945-288-2	US-08-462-831-2	US-08-461-809-2	US-08-461-441-2	US-08-482-142-2	US-08-478-572-2	US-08-484-296-2	PCT-US93-08518-2	US-07-945-288-10	US-08-462-831-10	US-08-461-809-10	US-08-461-441-10	PCT-US93-08518-10	US-07-945-288-11	US-08-462-831-11	US-08-461-809-11	US-08-461-441-11	PCT-US93-08518-11	US-08-460-040-2	US-07-945-288-6	US-08-462-831-6	US-08-461-809-6	US-08-461-441-6	US-08-482-142-6	US-08-478-572-6	US-08-484-296-6	PCT-US93-08518-6
	Length DB	245 1	245 1	245 1	245 1	245 2	245 2	245 3	245 5	320 1	320 1	320 1	320 1	320 5	222 1	222 1	222 1	222 1	222 5	245 3	321 1	321 1	321 1	321 1	321 2	321 2	321 3	321 5
مين	Query Match I	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	97.6	97.6	97.6	97.6	97.6	94.9	82.7	82.7	82.7	82.7	82.7	82.7	82.7	82.7
	Score	1206	1206	1206	1206	1206	1206	1206	1206	1206	1206	1206	1206	1206	1177	1177	1177	1177	1177	1144	997.5	997.5	997.5	997.5	997.5	997.5	997.5	997.5
	Result No.	1	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

Sequence 195, App Sequence 195, App	Sequence 195, App Sequence 197, App	Sequence 197, App Sequence 197, App	Sequence 2, Appli Sequence 20, Appl	4,	Sequence 4, Appli	Sequence 1, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 36, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli
US-08-482-142-195 US-08-478-572-195	US-08-484-296-195 US-08-482-142-197	US-08-478-572-197 US-08-484-296-197	US-08-330-121B-2 US-08-852-807-20	US-08-964-308-4	US-08-964-313-4	US-08-860-255A-1	US-09-069-138-4	US-08-915-095A-2	US-08-798-096-2	US-08-684-932A-36	US-08-798-095A-2	US-09-953-956-2	US-08-553-125A-2
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181	181	181	329	328	325	325	329	325	326	325	325	329	
30.9	30.9 29.4	2.00 4.4.	26.8	26.8	26.8	26.8	26.8	26.8	26.8	26.8	26.8	26.8	26.8
372.5 372.5	372.5	354.5	323.5	323.5	323.5	323.5	323.5	323.5	323.5	323.5	323.5	323.5	323.5
28 29	30 31	332	6. E.	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Length 245;
                                                                                                                                                                                                                                                                             COUNTRY:

ZIP:
USA
ZIP:
USA
ZIP:
USA
ZIP:
USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION UNDER: US/O7/945,288
FILING DATE: 19920910
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION UNDER: 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION UNDER: 580,655
FILING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: P36,207
REFERENCE/POCKET NUMBER: P36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 1206; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 222; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 245 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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JS-07-945-288-2
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Gaps

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Indels

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PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                      121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                144 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 TNACSINGNAPABIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 245;
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                                                                                                                                                                                       204 QGVDYMIVRNSWDTNWGDNGYGYFAAANIDLMMIEEYPYVVIL 245
                                                                                                                                                             181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: USA

ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,809
FLING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US/08/461,809
FILING DATE: 10 SEPTEMBER 1992
APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, AWY E.
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1PC-010CC (IMI-024)
TELECOMMONICATION INFORMATION:
TELECOMMONICATION NUMBER: 227-7400
TELEFRAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE: CLARACTERISTICS:
TENNOMATION FOR SEQ ID NO: 2:
TENNOMATION FOR SEQ ID NO: 2:
TENNOMATION FOR SEQ ID NO: 2:
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Pred. No. 1.4e-129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 60 STATE STREET, SUITE 510 CITY: BOSTON STATE: MA COUNTRY: USA ZIE
                                                                                                                                                                                                                                                                                                                                                                                                                                       DERMATOPHAGOIDES
                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08461809
Patent No. 5770202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
TITLE OF INVENTION: T CE
TITLE OF INVENTION: DERW
NUMBER OF SEQUENCE: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-809-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 JS-08-461-809-2
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                                                                                           61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                     121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                            24 TNACSINGNAPAEIDLROMRIVIPIRMOGGGGSCWAFSGVAATESAYLAHRNOSLDLAEO 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08462831
| Patent No. 5552142
| GENERAL INFORMATION:
| APPLICANT:
| TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM TITLE OF INVENTION: DERMATOPHAGOIDES NUMBER OF SEQUENCES: 13
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: LAHIVE & COCKFIELD STREET: 60 STATE STREET, SUITE 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1206; DB 1; Length 245; 100.0%; Pred. No. 1.4e-129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                      204 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 245
                                                                                                                                                                                                                                                                          181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIPECATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/945,288
FILING DATE: 10 SEPTEMBER 1992
APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 48,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MANDRAGOURAS, ANY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET UNMBER: 1PK
TELECOMMUNICATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 222; Conservative
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MOLECULE TYPE: protein
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CITY: BOSTON
STATE: MA
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ZIP: 02109
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US-08-462-831-2
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US-08-482-142-2
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144 PPNANKIREALAQTHSAIAVIIGIKULDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T CELL EPITOPES OF THE MAJOR ALLERGENS FROM DERMATOPHAGOIDES
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                                                                       181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                            204 QGVDYMIVRNSWDTNWGDNGYGYFAANIDLAMIEEYPYVVIL 245
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APPLICATION NUMBER: US 580,655
FILLING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILLING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/POCKET NUMBER: 1PC-010CC (IMI-024)
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION 1017 227-7400
TELEFONMUNICATION 1017 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           RESULT 4
US-08-461-41-2
Sequence 2, Application US/08461441
Fatent No. 5773002
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF LINGENTION:
TITLE OF LINGENTION:
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TITLE OF LINGENTION:
TITLE OF LANGINGES:
TITLE OF SEQUENCES:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy
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STATE: MA
COUNTRY: USA
TE: 02109
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84 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 143
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                                                                                                                                                                                            APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
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ADDRESSEE: IMMULGGIC PHARMACEUTICAL CORPORATION STREET: 610 LINCOLN STREET
CITY: WALTHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1206; DB 2;
100.0%; Pred. No. 1.4e-129;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT TYPE: Floppy disk COMPUTER: IBM PC COMPACIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII TEXT CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/482,142 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICE APPLICATION 1973
PRICE APPLICATION NUMBER: US/08/445,307
PILING DATE: 07 June 1995
ATTORNEY AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US
TELECOMMUNICATION INFORMATION:
Sequence 2, Application US/08482142
Patent No. 5820862
GENERAL INFORMATION:
                                                                                     Greenstein, Julia
Kuo, Mei-chang
Rogers, Bruce
Franzen, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (617) 466-6000
                                                                   Richard
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
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Best Local Similarity 100.0
Matches 222; Conservative
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APPLICANT: 1
APPLICANT: 0
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2, Application US/08484296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 PPNANKIREALAQTHSAIAVIIGIKOLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 83
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                                                     Sequence 2, Application US/08478572

Fatent No. 596856

GENERAL INPORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Chen, Xian
APPLICANTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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ZIP: 02154
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,572
FILING DATE: 07-Unne-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/445,307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE 1.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 466-6000
TELEFAX: (617) 466-6000
TELEFAX: (617) 466-6000
TELEFAX: (617) 466-6000
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 245 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                   JS-08-478-572-2
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RESULT 7 US-08-484-296-2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
APPLICANT: Garman, Richard
APPLICANT: Garman, Julia
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Kuo, Mei-chang
APPLICANT: Franzen, Henry
APPLICANT: Franzen, Henry
APPLICANT: Franzen, Henry
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL BPITOPES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: T CELL BPITOPES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: T CELL BPITOPES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: PROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSE: IMMULÇGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 1206; DB 3; Best Local Similarity 100.0%; Pred. No. 1.4e-129; Matches 222; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII FEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE:
CLASSIFICATION: 435
PION APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 07 June 1995
ATTORNEY AGENT INFORMATION:
NAME: CRAIG, ANNE I.
RECISTRATION UNMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US
TELECHMUNICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELECHMONE: (617) 466-6040
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS9308518; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-296-2
                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02154
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                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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USA
                      02109
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ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGGGSCWAPSGVAATESAYLAHRNQSLDLAEQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 TNACSINGNAPAEIDLRQMRTVTPIRMQGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Sequence 10, Application US/07945288

Parent No. 5433948

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET; SUITE 510
CITY: BOSTON
   T CELL EPITOPES OF THE MAJOR ALLERGENS FROM DERMATOPHAGOIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1206; DB 5; Length 245; 100.0%; Pred. No. 1.4e-129; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 QGVDYWIVRNSWDTNWGDNGYGYFAAANIDIAMHIEEYPYVVIL 245
                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08518
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/945,288
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/945,288
FILING DATE: 10 SEPTEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, ANY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1PC-010CC (IMI-024)
TELECHONE: (617) 227-7400
TELECHONE: (617) 227-7401
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TITLE OF INVENTION: T CELL EPITOPES C
TITLE OF INVENTION: DERNATOPHAGOIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                USA
                                                                                                                           STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US93-08518-2
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99 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAPSGVAATESAYLAHRNQSLDLAEQ 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TNACSINGNAPAEIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEO
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Patent No. 5552142
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
TITLE OF INVENTION: DERMATOPHAGOIDES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/945,288
FILING DATE: 19920910
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY AGENT INPORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: P36,207
REFERENCE/DOCKET NUMBER: P36,207
REFERENCE/DOCKET NUMBER: P36,207
TELECOMMUNICATION INPORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1206; DB 1;
100.0%; Pred. No. 2.1e-129;
tive 0; Mismatches 0;
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STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 320 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-07-945-288-10
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MEDIUM TYPE: Floppy
COMPUTER READABLE FORM:
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STATE: MA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 278
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US-08-461-809-10
Sequence 10, Application US/08461809
Fatent No. 5770202
FATEL OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: & CO STATE STREET, SUITE 510
CITY: BOSTON
STATE: MANON
ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLAMIEEXPYVVIL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,831
FILING DATE:
PRICA SIFICATION: 424
PRICA APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 690,655
FILING DATE: 10 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 37 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1PC-010CC (IMI-024)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ 1D NO: TELEFALL (617) 227-5941
SEQUENCE CHRARATERISTICS:
SEQUENCE CHRARATERISTICS:
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ZIP: 021.05A
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,809
FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-462-831-10
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99 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRIIIQRDNGYQPNYHAVNIVGYSNA 180
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| Patent No. 5773002
| GENERAL INFORMATION:
| APPLICANT:
| TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM TITLE OF INVENTION: DEMATOPHAGOIDES
| VORBESPONDENCES: | CORRESPONDENCES: ADDRESS: ADDRESSE: LAHIVE & COCKPIELD STREET: 60 STATE STREET; SUITE 510
| CITY: BOSTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1206; DB 1;
100.0%; Pred. No. 2.1e-129;
tive 0; Mismatches 0;
                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/945,288
FILING DATE: 10 SEPTEMBER 1992
APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
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APPLICATION NUMBER: US/08/461,441
APFLICATION NUMBER: 1992
PILING DATE: 10 SEPTEMBER 1992
APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY AGENT INFORMATION:
NAME: MANDEAGURAS, AMY E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity 100.0
Matches 222; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 PPNANKIREALAQTHSAIAVIIGIKOLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
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NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE $10
CITY: BOSTON
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1206; DB.1; Length 320; 100.0%; Pred. No. 2.1e-129; Live 0; Mismatches 0; Indels 0
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APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, ANY E
REGISTRATION NUMBER: 36,207
FEFERCE/COCKET NUMBER: 1PC-010CC (IMI-024)
TELECOMMUNICATION INFORMATION:
TELEFENNE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/945,288
APPLICATION NUMBER: US 07/945,288
ATTORNEX/AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1PC-010CC (IMI-024)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
PCT-US93-08518-10
; Sequence 10, Application PC/TUS9308518
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 222; Conservative
                                                                                                                                                                                                                                                                                      TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-461-441-10
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61 BLVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TNACSINGNAPAEIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEO
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| Sequence 11, Application US/07945288 |
| Patent No. 5433948 |
| Patent No. 5433948 |
| Patent No. 5433948 |
| SEMENAL INFORMATION: |
| APPLICANT: Thomas, Wayne R. |
| APPLICANT: Chuas, Wayne R. |
| TITLE OF INVENTION: CLONING AND SEQUENCING OF ALLERGENS FROM |
| TITLE OF INVENTION: DERMATOPHAGOIDES (HOUSE DUST MITES) |
| NUMBER OF SEQUENCES: 13 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: LAHIVE & COCKFIELD |
| STREET: 60 STATE STREET, SUITE 510 |
| CITY: BOSTON |
| STREET: ANA |
| STREE
                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 1206; DB 5; Length 320; Best Local Similarity 100.0%; Pred. No. 2.1e-129; Matches 222; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
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CLASSIFICATION: 514
PRICIA APPLICATION DATA:
APPLICATION NUMBER: 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY AGENT TRFORMATION:
NAME: MANDRAGGURAS, AMY E.
REGISTRATION NUMBER: 195,207
REFERENCE/DOCKET NUMBER: 19C-010CC (IMI-024)
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INPORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/945,288
FILING DATE: 19920910
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
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TYPE: AMINO ACID
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                                                                                                                                                                                      MOLECULE TYPE: protein PCT-US93-08518-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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Search completed: May 19, 2005, 17:32:32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 PPNXNKIREALAQTHXAIAVIIGIKDLDAFRHYDGRTTIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGGSCWAFSGVAATESAYLAXRNQSLDLAEQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
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                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 215
CTHER INFORMATION: /label=Xaa is Glu or Gln US-07-945-288-11
                  LOCATION: 50
OTHER INFORMATION: /label=Xaa is His or Tyr
                                                                                                          LOCATION: 81
OTHER INFORMATION: /label=Xaa is Glu or Lys
                                                                                                                                                                                                 LOCATION: 124
OTHER INFORMATION: /label-xaa is Ala or Val
                                                                                                                                                                                                                                                                                       LOCATION: 136
OTHER INFORMATION: /label=Xaa is Ser or Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: T CELL EPITOPES OF TITLE OF INVENTION: DERMATOPHAGOIDES NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/945,288
FILING DATE: 10 SEPTEMBER 1992
APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08462831
Patent No. 5552142
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature LOCATION: 215
NAME/KEY: misc feature
                                                                                                                                                                            NAME/KEY: misc feature
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                                                                                   NAME/KEY: misc feature
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Florm:
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61 ELVDCASQHGCHGDTIPRGIXY1QHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
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97.7%; Pred. No. 2.5e-126;
Live 0; Mismatches 5; Indels
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FILING DATE: 13 FEBRUARY 1990

ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGURAS, AMY E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1PC-010CC (IMI-024)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-7400
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 81
OTHER INFORMATION: /label=Xaa is Glu or Lys
                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 50
OTHER INFORMATION: /label=Xaa is His or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 215
OTHER INFORMATION: /label=Xaa is Glu or Gln
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OTHER INFORMATION: /label=Xaa is Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /label=Xaa is Ala
                                                                                                                                                                                                                 TOPOLOGY: 1:00.000
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LOCATION: 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-462-831-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 19, 2005, 17:39:08 ; Search time 39 Seconds (without alignments) 547.695 Million cell updates/sec Run on:

US-09-867-159A-2 1206 1 TNACSINGNAPAEIDLRQMR.....YFAANIDLMMIEEYPYVVIL 222

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

114359 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 222

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

4 [11000		* 2			SUMMARIES	
No.	Score	Match	Match Length	8	ΙD	Description
¦	982.5	81.5	211	7	\$21864	ι (Co
7	389.5	32.3	94		S03380	major fecal allerg
m	315	26.1	215		A59428	
4	311	25.8	221		A59041	cysteine proteinas
'n	301	25.0	216		806837	Ō.
9	298	24.7	218		KHCHL	cathepsin L (EC 3.
7	295	24.5	221	~	A59040	cysteine proteinas
00	284.5	23.6	217		S15844	cathepsin S (EC 3.
σ	274	22.7	214		S46476	cysteine proteinas
10	273	22.6	218		S67481	
11	240	19.9	212		S03964	stem bromelain (EC
12	209	17.3	183		A44938	cysteine proteinas
13	207	17.2	184		S02729	actinidain (EC 3.4
14	185.5	15.4	166		B44938	cysteine proteinas
15	179		95	7	PQ0650	senescence-associa
16	171		165		C44938	cysteine proteinas
17	156.5	13.0	139		A41404	cathepsin L (EC 3.
18	145		174	7	B48454	cathepsin B-like c
19	139	11.5	155		S57426	cysteine proteinas
20	129.5	10.7	110		A61061	actinidain (EC 3.4
21	129.5	10.7	157		S57451	
22	125.5	10.4	136		5762	
23	123.5	10.2	152		S57425	cysteine proteinas
24	121	10.0	150		T25581	hypothetical prote
25	120.5		152		S57423	cysteine proteinas
56	116.5	٠	152		5742	cysteine proteinas
27	115	9.5	145		S60456	cysteine proteinas
28	111.5	•	30		276	major fecal allerg
53	111	9.5	152		S57422	cysteine proteinas

NyAlternate names: allergen Der pl - house-dust mite (Dermatophagoides pteronyssinus) (fragmen NyAlternate names: allergen Der pl Cispecies: Dermatophagoides pteronyssinus (Cispecies: Dermaterophagoides pteronyssinus Cispecies: Dermatophagoides pteronyssinus Cipate: 05-Mar-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004 Ciscession: 803380 R.S.; Note, E.C.; Moritz, R.L.; Stewart, G.A. Protein Sog. Data Anal. 2, 17-21, 1989 Protein Seq. Data Anal. 2, 17-21, 1989 Protein Seq. Data Anal. 2, 17-21, 1989 A;Title: Structural studies on the allergen Der pl from the house dust mite Dermatophago A;Reference number: A31657; MUID:89098855; PMID:2911558

RESULT 2

major fecal allerg	cathepsin B-like c	cysteine proteinas	cysteine proteinas	probable cysteine	cysteine proteinas	cysteine proteinas	cysteine proteinas	cysteine proteinas	cruzipain (EC 3.4.	dipeptidy1-peptida	cysteine proteinas	cysteine proteinas	hypothetical prote	cysteine proteinas	cysteine proteinas
A27634	A29172	T37284	B26074	T05920	T02166	835577	T08595	B48566	S16162	\$23941	S35580	S35578	T51569	S57427	S41426
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30 2	73 2	133 2	96 2	91 2	156 2	43	82	149 2	173 2	119 2	43 2	43 2	112 2	152 2	100
8.8 30 2	8.8 73 2														
106.5 8.8 30 2	8.8	8.7	8.7		8.1			7.4				7.0	8.9		9.9

ALIGNMENTS

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RESULT 1 S21864 probable cysteine proteinase (EC 3.4.22) - Euroglyphus maynei probable cysteine proteinase (EC 3.4.22) - Euroglyphus maynei NiAlternate names: allergen Eur m I Cispecies: Euroglyphus maynei Cibace: 20-Feb-1995 #text_change 09-Jul-2004 Cibacesion: S21864 Rikent, N.A.; Hill, M.; Keen, J.N.; Holland, P.W.H.; Hart, B. A;Reference number: S21864 A;Reference number: S21864 A;Accassion: S21864 A;Accassion: S21864 A;Accassion: S21864 A;Accassion: S21864 A;Accassion: S21864 A;Reference number: S21864 A;Accassion: S21864 A;Accassion: S21864 A;Accassion: S21864 A;Accassion: S21864 A;Reference number: S21864 A;Accassion: S21864 A;Accassion: S21864 A;Accassion: S21864 A;Accassion: S21864 A;Accassion: Cysteine proteinase; hydrolase	Query Match 81.5%; Score 982.5; DB 2; Length 211; Best Local Similarity 83.3%; Pred. No. 4.3e-81; Matches 177; Conservative 17; Mismatches 16; Indels 1; Gaps 1;	1 TNACSING-NAPAEIDLRQWRTVTPIRMQCGCGSGWAFSGVAATESAYLAHRNQSLDIAE 59	60 QELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQI 119 	120 YPPNANKIREALAQTHSALAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSN 179 :: :	180 AQGYDYWIYRNSWDTWWGDNGYGYFAANIDL 210
RESULT S21864 S21864 S21864 N.Alte C; Spec C; Acce R; Refe A; Refe A; Resi- A; Resi- A; Cene A; Cene C; Gene C; Gene C	M Be	ç q	S G	8 S	55 d

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Length 221;

63

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A; Description: Amino acid sequences of cysteine proteases from ginger rhizome, Zingiber
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 GCRGGWMNPAFQFIVNNGGINSETYPYRGQDGICNSTVNAPVVSIDSYENVPSHNEQSL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 REALAQTHSAIAVIIGIKDLDAFRH--YDGRTIIQRDNGYQPNYHAVNIVGYSNAQGVDY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 QKAVANQPVSVTWDAAGRDFQLYRSGIFTGSCNISAN-----HALTVVGYGTENDKDF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 PAEIDLROMRIVIPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDC-ASQH'69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 PDSIDWRENGAVVPVKNQGGCGSCWAFSTVAAVEGINQIVTGDLISLSEQQLVDCTTANH
                                                                                                          A; Accession: 459041
A; Accession: 459041
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-221 < cLAU>
A; Residues: 1-221 < cLAU>
A; Residues: 1-221 < cLAU>
A; Cross-references: UNIPROT: P82474
A; Experimental source: thizome
C; Superfamily: papain
C; Reywords: cysteine proteinase; glycoprotein; hydrolase
F; 24-65, 58-98, 155-206/Disulfide bonds: #status experimental
F; 27, 161, 181/Active site: Cys, His, Asn #status predicted
F; 99, 156/Binding site: carbohydrate (Asn) (covalent) #status experimental
       C,Accession: A59041
R,Laursen, R.A.
submitted to the Protein Sequence Database, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                25.8%; Score 311; DB 2; 33.8%; Pred. No. 1.4e-20; ive 34; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||:||| |||:||
177 WIVKNSWGKNWGESGYIRAERNIE 200
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 33.8%,
Matches 69, Conservative
                                                                                                 A; Reference number: A59041
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                                                                                                                                                                                                                                                           58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ervatamin B (EC 3.4.22.-) - Ervatamia coronaria
C;Species: Brvatamia coronaria
C;Species: Brun-2002 #sequence_revision 21-Jun-2002 #text_change 09-Jul-2004
C;Accession: A59428
R;Dattagupta, J.K.
Submitted to the Protein Sequence Database, May 2002
A;Reference number: A59428
A;Reference number: A59428
A;Reference number: A59428
A;Reference number: Preliminary
A;Rolecule type: preliminary
A;Rolecule type: protein
A;Residues: 1-215 < DAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cysteine proteinase II (EC 3.4.22.-) - ginger
C;Species: Zingiber officinale (ginger)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                         1 TNACSINGNAPABIDLRQMRTVTPIR--MQGGCGSCWAFSGVAATESAYLAHRNQSLDLA
                                                                                                                                                                                                                                                                                                                                                 59 EQELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQELVDC-ASQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSFVDWRSKGAVNSIKNOKOCGSCWAFSAVAAVESINKIRTGOLISLSEQELVDCDTASH
                                                                                                                                                                                                                                                                                 1 TNACSINGNAPAEIDLRQMRTVTPIRMQMQGGCGSXXAFSGVA-------
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                              89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                   DB 2; Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 215;
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YWIVRNSWDTNWGDNGYGYFAANI-----DLMMIEEYP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GIEYIQHNGVVQESYY----
                                                                                                                                                                 Score 389.5; DB 2,
Pred. No. 4.2e-28;
0; Mismatches 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 315; DB 2;
Pred. No. 5.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:P60994
A,Note: plant cysteine protease, plant latex
C,Keywords: cysteine proteines; hydrolase
F;22-63,56-96/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.1%; Scott 34.5%; Pred. No. 5.
A;Accession: S03380
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28;29-43;44-60;61-76;77-94 <SIM>A;Cross-references: UNIPROT:Q7M431
C;Superfamily: papain
                                                                                                                                                            ch 32.3%;
l Similarity 48.6%;
88; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 34.5
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYPPNANK----
                                                                                                                                                               Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 N 179
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A; Accession: S06837
A; Molecule type: protein
A; Residues: 1-216 < RIT>
A; Mockey R: Mockey R: Matchews, J.A.; Smith, C.J.; Smith, H.
B; Mockey R.A.; Adams, S.; Matchews, J.A.; Smith, C.J.; Smith, H.
B; Mockey R.A.; Adams, S.; Matchews, J.A.; Smith, C.J.; Smith, H.
B; Mockey R: Molecular cloning of two cysteine proteinases from paw-paw (Carica papaya).
A; Molecular Cloning of two cysteine proteinases from paw-paw (Carica papaya).
A; Accession: A26074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 155-216 <MCK>
A; Cross-references: GB:X03970; GB:M24252; NID:g18087; PIDN:CAA27608.1; PID:g18088
C; Superfamily: papain
C; Keywords: cysteine proteinase; hydrolase
F;22-63;56-95,153-204/Disulfide bonds: #status predicted
F;25,159,179/Active site: Cys, His, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
glycyl endopeptidase (EC 3.4.22.25) - papaya
N;Alternate names: papaya peptidase B; papaya proteinase IV
C;Species: Carlos papaya (papaya)
C;Daces: 30-Sep.1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S06837; A26074
R;Ritonja, A.; Buttle, D.J.; Rawlings, N.D.; Turk, V.; Barrett, A.J.
FEBS Lett. 258, 109-112, 1989
A;Title: Papaya proteinase IV amino acid sequence.
A;Reference number: S06837; MUID:90076470; PMID:2591528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 PARIDLROMRIVIPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEOELVDCASQ-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PESVDWRAKGAVTPVKHQGYCESCWAFSTVATVEGINKIKTGNLVELSEQELVDCDLQSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
25.0%; Score 301; DB 2;
Best Local Similarity 34.0%; Pred. No. 1.1e-19;
Matches 67; Conservative 37; Mismatches 79
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A;Experimental source: rhizome
A;Note: residues 80-87 were not determined but are based on mass measurement and similar
C;Superfamily: papain
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A. Residues: 1-277 - KRT.
A. Residues: 1-277 - KRT.
A. Cross-references: UNIPROT: P25326
R. Wiederanders, B.; Broemme, D.; Kirschke, H.; Kalkkinen, N.; Rinne, A.; Paquette, T.; T
R. Wiederanders, B.; Broemme, D. Kirschke, H.; Kalkkinen, N.; Rinne, A.; Paquette, T.; T
A. Title: Primary structure of bovine cathepsin S. Comparison to cathepsins L, H, B and p
A. Reference number: S16972; MUID: 91323515; PMID: 1864368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: The complete amino acid sequence of bovine cathepsin S and a partial sequence o A;Reference number: S15844; MUID:91257334; PMID:2044774
                                                                                                                                                                                                                                                                                                              R;Laursen, R.A.
submitted to the Protein Sequence Database, July 1999
A;Description: Amino acid sequences of cysteine proteases from ginger rhizome, Zingiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 GCHGDTIPRGIEYIQHN-GVVQESYYRYVAREQSC-RRPNAQRFGISNYCQIYPPNANKI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                            cysteine proteinase I (EC 3.4.22.-) - ginger
C;Species: Zingiber officinale (ginger)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: A59040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDSIDWREKGAVVPVKNQGGCGSCWAFDAIAAVEGINQIVTGDLISLSEQQLVDCSTRNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 PAEIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDCASQ-H
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A;Rebidues: 22-217 <MIE>
A;Cross-references: GB:M95211; NID:g162814; PIDN:AAA30435.1; PID:g162815
A;Note: 143-Pro was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: cysteine proteinase; glycoprotein; hydrolase
F;24-65,58-98 155-206/Disulfide bonds: #status predicted
F;27,161,181/Active site: Cys, His, Asm #status predicted
F;95,156/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91; Indels
KKYWIVKNSWGEKWGDKGYIYMAKDRKNHCGIATAASYPLV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.5%; Score 295; DB 2; Best Local Similarity 32.0%; Pred. No. 3.8e-19; Matches 65; Conservative 35; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: not compared with conceptual translation
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WTVKNSWGKNWGESGYIRVERNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molcoule type: protein
A;Residues: 1.-221 <LAU>
A;Cross-references: UNIPROT:P82473
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A59040
A;Accession: A59040
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178
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A; Residues: 1-20, I', 22-28, N', 30-39, F', 41-96, 99-108, K', 110-175;177-196, 'Q', 198-218 < C. Complex: heterodimer of disulfide linked chains produced from a single chain precursor C; Function:
A; Description: catalyzes hydrolysis of peptide bonds in proteins
A; Pathway: intracellular protein degradation
A; Pathway: intracellular protein degradation
A; Postoriar important role in the lysosomal degradation of proteins
C; Superfamily: papain
C; Keywords: cysteine proteinase; glycoprotein; heterodimer; hydrolase; liver; lysosome; C; Superfamily: papain
C; Keywords: cathepsin L heavy chain #status experimental < ACH>
F; 1.176-Product: cathepsin L light chain #status predicted
F; 218-207/bisulfide bonds: #status predicted
F; 25, 165, 185, Active site: Cys, His, Asn #status predicted
F; 109/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: S00081
A;Molecule type: protein
A;Residues: 1-176;177-218 <WAD>
R;Mada, K. 27 anabe, T.
FEBS Lett. 209, 330-334, 1986
A;Title: N-terminal amino acid sequences of the heavy and light chains of chicken liver
A;Reference number: A91372; MUID:87080783; PMID:3792553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                     A; Molecule type: protein
A;Reaidues: 1-37;177-216 < WAZ>
A;Reaidues: 1-37;177-216 < WAZ>
R;Dufour, E.; Obled, A.; Valin, C.; Bechet, D.; Ribadeau-Dumas, B.; Huet, J.C.
Biochemistry 26, 5689-5695, 1987
A;Title: Purification and amino acid sequence of chicken liver cathepsin L.
A;Reference number: A26818; MUID:88050863; PMID:3676277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 ANKIREALAQTHS-AIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- PNAORFGISNYCQIYPPNA 124
                                                                                                                                                                    NKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQGVD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cathepsin L (EC 3.4.22.15) - chicken
NyAlternate names: major excreted protein (MEP); procathepsin L
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 31-Mar-1992 #sequence revision 18-Oct-1996 #text_change 18-Mar-1997
C;Accession: S00081; A25654; Ā26818; B25654
R;Wada, K.; Takal, T.; Tanabe, T.
Rwada, K.; Takal, T.; Tanabe, T.
A;Takal, T.; Tanabe, T.
A;Title: Amino acid sequence of chicken liver cathepsin L.
A;Reference number: S00081; MUID:87304227; PMID:3305012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 APAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQELVDCA---
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                             GCHGDT1PRG1EY1QHNGVVQESYYRYVAREQSCRR-
                                                                                                                                                                                                                                                                                                                                               174 YILIKNSWGPGWGENGY 190
                                                                                                                                                                                                                                                                                                           185 YWIVRNSWDTNWGDNGY 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A25654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A26818
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Cipate: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Apr-2000 C;Accession: S67481 #sequence_revision 25-Apr-1997 #text_change 20-Apr-2000 C;Accession: S67481 #sequence_revision S; Emori, Y. Riatanaber. 227, S82-587, 1995 A;Title: A putative digestive cysteine proteinase from Drosophila melanogaster is predomn! A;Reference number: S67481; MUID:95154345; PMID:7851441 A;Accession: S67481 A;Ac
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RRItonja, A.; Rowan, A.D.; Buttle, D.J.; Rawlings, N.D.; Turk, V.; Barrett, A.J.
RRItonja, A.; Rowan, A.D.; Buttle, D.J.; Rawlings, N.D.; Turk, V.; Barrett, A.J.
RITOLS Lett. 247, 419-424, 1989
A.Title: Stem bromelain: amino acid sequence and implications for weak binding of cystatis
A.Feference number: S03964; MUID:89232167; PMID:2714443
A.Reference number: S03964; MUID:89232167; PMID:2714443
A.Residues: 1-212 - RIIT>
A.Residues: 1-212 - RIIT>
A.Cross-references: UNIPROT:P14518
C.Superfamily: papain
C.Superfamily: papain
C.Superfamily: papain
                                                                                                                                                                               (Drosoph
                                                                                                                                                                               (EC 3.4.22.-) CPl [similarity] - fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ģ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 KMPEPVPTVGPVSVAIDASH-ESFQFYSEGVYNEPQCDAQNLDHGVLVVGFGTDESGEDY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 CHGDTIPRGIEYIQHN-GVVQESYYRYVAREQSCRR---PNAQRFGISNYCQIYPPNANK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70
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C;Species: Ananas comosus (pineapple)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 --GCHGDTIPRGIEYIQHNGVVQ-ESYYRYVAREOSCRRPNAQRFGISNYCQIYPPNANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 NNGCNGGLMDNAFPYIKDNGGIDTEKSYPYEAIDDSCHFNRAQVGATDRGFTDIPQGDEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 PAEIDLRQMRŢVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQELVDCASQH-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Superfamily: papain
C,Keywords: cysteine proteinase, hydrolase
F,25,164,185/Active site: Cys, His, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Match 19.9%; Score 240; DB 2; L. Local Similarity 31.2%; Pred. No. 3.2e-14; les 63; Conservative 32; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.6%; Score 273; DB 2;
llarity 32.7%; Pred, No. 3.5e-17;
Conservative 28; Mismatches 98
                                                                                                                                                                                   cathepsin L-like cysteine proteinase
                                                                                                                                                                                                                   C;Species: Drosophila melanogaster
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181 WLVKNSWGTTWGDKGF 196
          186
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          LIKNSWGPXWGEXGY
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Best Local S:
Matches 63
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A;Molecule type: protein
A;Residues: 1-214 <JAZJ.
A;Residues: 1-214 <JAZJ.
A;Azziri, M.; van Beeumen, J.; Schnek, A.G.; Kleinschmidt, T.; Looze, Y.
Biol. Chem. Hoppe-Seyler 374, 501-506, 1993
A;Title: Isolation and preliminary characterization of the cysteine-proteinases from the A;Reference number: S35577; MUID:94030669; PMID:8216902
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C;Species: Carica pubescens (mountain papaya)
C;Species: Carica pubescens (mountain papaya)
C;Aate: 15-Jul-1995 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
C;Aacession: 846476; S35579
R;Jaziri, M.; Kleinschmidt, T.; Walraevens, V.; Schnek, A.G.; Looze, Y.
Biol. Chem. Hoppe-Seyler 375, 379-385, 1994
A;Title: Primary structure of CC-III, the glycosylated cysteine proteinase from the A;Reference number: S46476; MUID:95071624; PMID:7980869
                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -OHGCHGDTIPRGIEY-IQHNGVVQESYYRYVAREQSCRRPNAORFG-ISNYCQIYPPNA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNY-HAVNIVGYSNAQGV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQR--FGISNYCQIYPPNANK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ::|:: | || || || ISLIKAIAKQPVSVLVESKG-KAFQFYK-KGIFGGPCGTKVD-HAVTAVGY----GKDY1 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GNKGCNGGFMTEAFQYIIDNNGIDSEASYPYKAMDGKCQYDVKNRAATCSRYIELPFGSE 121
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F;1-214/Product: cystaine proteinase III #status experimental <MAT>
F;22-63,56-95,153-200/Disulfide bonds: #status predicted
F;25,159,175/Active site: Cys, His, Asn #status predicted
F;44/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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                                                                                                                                                                                                            DB 2; Length 217;
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A;Residues: 1-28;48-71;94-104;107-131;146-162;178-217 <W12> C;Superfamily: papain C;Kypwords: crysteine proteinase; hydrolase F;12-110,22-66,56-99,158-206/Disulfide bonds: #status predicted F;25,164,184/Active site: Cys, His, Asn #status predicted
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                                                                                                                                                                                                                                                                                91; Indels
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A, Molecule type: protein
A, Residues: 1-21, 'X', 23-24, 'X', 26-43 < WAL>
A, Note: the source is designated as Carica candamarcensis
C, Superfamily: papain
                                                                                                                                                                                                                                                    .2e-18;
                                                                                                                                                                                                            Query Match
23.6%; Score 284.5;
Best Local Similarity 33.8%; Pred. No. 3.2e
Matches 69; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYWIVRNSWDTNWGDNGYGYFAAN 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 IVRNSWDTNWGDNGY 201
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Cysteine proteinase (EC 3.4.22.-) - Trypanosoma brucei (fragment)
Cysteine proteinase (EC 3.4.22.-) - Trypanosoma brucei
Cysteine 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
CyAccesion: B44938
CyAccesion: B44938
Alitle: Amplification and sequencing of genomic DNA fragments encoding cysteine proteas
Alitle: Amplification and sequencing of genomic DNA fragments encoding cysteine proteas
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Aliterance preliminary; nucleic acid sequence not shown; not compared with conceptual tra
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R;Hensel, Li., Gtblic, V.; Baumgarten, D.A.; Bleecker, A.B.
Blant Cell 5, 553-564, 1993
A;Title: Developmental and age-related processes that influence the longevity and senesc A;Reference number: PQ0650; MUID:93299122; PMID:8518555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                        61 WALQTAVTYQPVSVALDAAG-DAFKHYSSGIFTGPCGTAID------HAVTIVGYGT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G--VVQESYYRYVA--REQSCRRPNAQRFG--ISNYCQIYPPNANKIREALAQTHS-AIA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GGNVFTEASYPYVSGNGEÖPQCQMNGHEIGAAITDHVDL-PQDEDAIAAYLAENRPLAIA 119
                                     127 IREALAQTHSAIAVIIGIKDLDAFRHYDG-----RTIIQRDNGYQPNYHAVNIVGYSN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QGQCGSCWAFSTIGNIEGQWQVAGNPLVSLSEQILVYCDPLIGCGGGLMDNAFNWIVNSN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              senescence-associated protein SAG2 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDCASQHGCHGDTIPRGIEYI-QHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V----EAPQFYGHNGGYILTSCTSEQLD-HGVLLVGYNDNSNPPYWIVKNSW 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 VIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQGVDYWIVRNSW 192
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A;Residues: 1-95 «HEN»
A;Cross-references: UNIPROT:Q91L83
C;Coment: This protein is a senescence-associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Superfamily: papain
C, Keywords: cysteine proteinase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 58; Conserv
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Best Local Similarity
Matches 38; Conserv
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C;Superfamily: papain
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Cysteine proteinase (EC 3.4.22.-) - Trypanosoma cruzi (fragment)
Cysteine proteinase (EC 3.4.22.-) - Trypanosoma cruzi (fragment)
C;Species: Trypanosoma cruzi
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A44938
Mol. Biochem. Parasitol. 39, 1-8, 1990
A;Title: Amplification and sequencing of genomic DNA fragments encoding cysteine proteas
A;Reference number: A44938
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molacule type: DNA
A;Residues: 1-183 *EAKs
A;Residues: 1-183 *EAKs
A;Cross-references: UNIPROT:Q9GPN3; UNIPROT:Q8T2Y4; UNIPROT:Q26883; UNIPROT:Q26884; GB:MC;Superfamily: papain
C;Superfamily: papain
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C;Species. Actinidia chinensis (kiwi fruit)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Jun-1999
C;Accession: 802729
R;Praekelt, U.M.; McKee, R.A.; Smith, H.
Balant Mol. Biol. 10, 133-202, 1988
A;Title: Molecular analysis of actinidin, the cysteine proteinase of Actinidia chinensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                            GCHGDTIPRGIEYIQHNGVVQ-ESYYRYVAREQSCR--RPNAQRFGISNYCQIYPPNANK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 HGCHGDTIPRGIEYI---QHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIYPPNAN 125
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127 IREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQGVDYW 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 KI---REALAQTHSAIAVIIGIKDLDAFRH-----YDGRTII-----QRDNGYQPNYHA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 APAEIDLRQMRTVTPIRMQGGGGSCWAFSGVAATESAYLAHRNQSLDLAEQELVDC-ASQ 68
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                                                                                                                                          IVRNSWDTNWGDNGYGYFAANI 208
                                                                                                                                                                                   171 IYPKKWGAKWGEAGYIRMARDV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 UNIVGYSNAQGVDYWIVRNSW 192
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163 LLLVGYNDSAAVPYWIVKNSW 183
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Matches 60; Conservative
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Best Local Similarity
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A, Molecule type: mRNA
A, Residues: 1-184 <PRA>
                                                                                                                                          187
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Acariformes, Sarcoptiformes, Astigmata, Psoroptidia, Analgoidea,
Pyroglyphidae, Dermatophagoides.
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Hao M.Q., Xu J., Zhong N.S.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

- !- SIMILARITY: Belongs to peptidase family Cl.

R EMBL; AF27634; AA7634.

R PIR; A27634; A27634.

R PIR; A27634; A27634.

R PIR; A27634; PRO00610; F: cysteine-type endopeptidase activity; IEA.

R PIR; PRO006109; P: peptidase_Cl.

R InterPro; IPR000668; Peptidase_Cl.

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R PRINTS; PR00112; Peptidase_Cl; T.

R PRNSTIE; PR00139; THIOL PROTEASE_ASN; 1.

R PROSITE; PS00649; THIOL PROTEASE_CYS; 1.

R PROSITE; PS00640; THIOL PROTEASE_CYS; 1.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Allergen Der fI (Fragment).
Dermatophagoides farinae (House-dust mite).
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Matches 171; Conservative
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Dermatophagoides pteronyssinus (House-dust mite).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea; Pyroglyphidae; Dermatophagoides.
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01-MAR-2004 (TEBBLrel. 26, Created)
01-MAR-2004 (TEBBLrel. 26, Last sequence update)
01-MAR-2004 (TEBBLrel. 26, Last annotation update)
01-MAR-2004 (TEBBLrel. 26, Last annotation update)
Major fecal allergen Der p I (Fragments).
Dermatophagoides pteronyssinus (House-dust mite).
Eukaryotes, Metazoas, Arthropoda, Chelicerata, Arachnida, Acari,
Acariformes, Sarcoptiformes, Astigmata, Peoroptidia, Analgoidea,
Pyroglyphidae; Dermatophagoides.
                                                                                                                                                                                     61 AIAVIIGIKDLRAFQHYDGRTIIQHDNGYQPNYHAVNIVGYGSTQGV 107
                                                                                                                                                                  137 AIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQGV 183
    Score 469; DB 2; Length 10
Pred. No. 2.5e-34;
8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 36.2%; Score 437; DB 2; Length 13 Best Local Similarity 61.4%; Pred. No. 2.4e-31; Matches 81; Conservative 17; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Park H., Yun H.C., Kim K.Y., Park S.Y., Park S.K.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; P60994, ARX38773.1; -.
HSSP; P60994, IMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 AA; 14965 MW; 5033C26B15E68E9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0008234; F:cysteine-type peptidase activity; GO; GO:0006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR000668; Peptidase_C1.
                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                    Created
                                                                                                                                                                                                                                                                                                          PRT;
      38.9%;
80.4%;
                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2003 (TrEMBLrel. 24,
Query Match
Best Local Similarity 80.49
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 RHYDGRTIIQRD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 RHYDGSYVITTD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6956;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7M431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIEYIQQNGVVEERSYPYVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVAATESAYLAHRNQSLDLAEQELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                         Dermatophagoides farinae (House-dust mite).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
Pyroglyphidae; Dermatophagoides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Acari,
Acariformes, Sarcoptiformes, Astigmata, Psoroptidia, Analgoidea,
Pyroglyphidae, Dermatophagoides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Indels
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Park H., Park S.K., Yun H.C.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF194431; AAL14424.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0008234; F:cysteine-type peptidase activity; IEA. GO; GO:0006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR000668; Peptidase_Cl.
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Park H., Park S.Y., Kim K.Y., Park S.K., Yun H.C.;
Submitred (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF194321, AAL14425.1;
INTERPTO; IPR000169; Pept cys acsite.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 AA; 16852 MW; BB304800946D4047 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12277 MW; A80E7876CBA6F97A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 607; DB 2;
Pred. No. 1.5e-46;
                                                                                                        146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 AA
    181 QGVDYWIVRNSWDTTWGDSGYGYFQAGNNL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dermatophagoides farinae (House-dust mite)
                                                                                                                                             Created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                      Cysteine proteinase (Fragment).
Name=CPW2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cysteine proteinase (Fragment).
Name=CPW3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF00112, Peptidase_C1, 1
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84.2%;
                                                                                                                                                                                     (TrEMBLrel. 24,
                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQRDNGYQPNYHA 171
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                                                                                                      PRELIMINARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                    095X05
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Q95X04
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Q95X05
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Length 133;

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11 PAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQELVDCASQ--
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                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 44, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to
PIR; A59428; A59428.
PDB; IIWD; X-ray; A=1-215.
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158
178
22
56
152
215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=52861;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fabernaemontana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Latex;
                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                          ERVB TABDI
P60994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coronaria.
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DISULFID
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 IYPPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYS 178
                                                                                                                                                                                                                                                                                                                                                                        TNACSINGNAPAEIDLRQMRTVTPIR--MQGGCGSCWAFSGVAATESAYLAHRNQSLDLA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 -----RFGISNYCQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                 ----- 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 IYPPNANK-----DNGYQPNYXAVNIVGYX 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                Simpson R.J., Nice E.C., Moritz R.L., Stewart G.A.; "Structural studies on the allergen Der pl from the house dust mite Dermatophagoides pteronyssinus: similarity with cysteine
                                                                                                                                                                                                                                                                                                                                     89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Acari,
Acariformes, Sarcoptiformes, Astigmata, Glycyphagoidea;
                                                                                                                                                                                                                                                                                             DB 2; Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.7%; Score 382; DB 2; Length 221; llarity 38.4%; Pred. No. 3.7e-26; Conservative 35; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                       proteinases.";
Proteinases.";
Proteinaseq. Data Anal. 2:17-21(1989).
PIK, 503380, 503380.
GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
GO; GO:0005508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000668; Peptidase_CI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mora C.I., Diaz A.M., Montealegre F., Flores I.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF277840; AAK58415.1; --
HSSP; P53634; IK3B.
                                                                                                                                                                                                                                                                                                                                                                                                  1 TNACSINGNAPAEIDLROMRIVIPIRMOMOGGGGSXXAFSGVA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cysteine protease.
272845E5A53F2900 CRC64;
                                                                                                                                                                                                                                                      94 AA; 10327 MW; 9BF744165C8428A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0004197; F:cysteine-type endopeptidase activ:
GO; GO:0006508; P:proteolysis and peptidolysis; IEA
InterPro; IPR000068; Peptidase_Cl.
InterPro; IPR000169; Pept cys acsite.
Pfam; PF00112; Peptidase_Cl; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                           Score 389.5; DB 2,
Pred. No. 2.9e-27;
0; Mismatches 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0705; PAPAIN.
SMART; SM00645; Pept C1; 1.
PROSITE; PS00139; THIOL PROTEASE CYS; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
MEDLINE=89098855; PubMed=2911558;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cysteine protease (Fragment).
                                                                                                                                                                                                                                                                                             32.3%;
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                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Echimyopodidae; Blomia.
NCBI TaxID=40697;
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Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                               Local Similarity
les 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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10 095 Pd.4

10 095 Pd.4

10 097 Pd.4

10 011 Pd.
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-----HGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQ--RFGISNYCQIY 120
                                                                                                                                      62 DPTYKCHGCQSGMSPEAFKYMKQKGLLEESHYPYKMKLNQC-QANARGTRYHVSSY---- 116
                                                                                                                                                                                                                                        PPNANKIREALAQTHSAI----AVIIGIKDLDA-FRHYDGRTIIQRDNGYQPNY--HAVN 173
                                                                                                                                                                                                                                                                                    05-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Ervatamin B (EC 3.4.22.-) (ERV-B).
Tabernaemontama divaricata (Crepe jasmine) (Ervatamia coronaria).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
Immids; Gentianales; Apocynaceae; Rauvolfioideae; Tabermontantaneae;
펎,
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Kundu S., Sundd M., Jagannadham M.V.;
"Purification and characterization of a stable cysteine protease
ervatamin B, with two disulfide bridges, from the latex of Brvatamia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Agric. Food Chem. 48:171-179(2000).
-!- FUNCTION: Cysteine protease.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Lattcifer.
-!- PTM: Not glycosylated.
-!- PTM: Not glycosylated.
-!- PTM: Ascalansous. Active over the pH range 3.0-10.5 and up to 62 degrees Celaius. Stable in 8 M urea and 2.5 M GuHCl at neutral in 40% acetonitrile, 70% ethanol and 50% methanol. Unstable in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Proposed amino acid sequence and the 1.63 A X-ray crystal structuce a plant cysteine protease, ervatamin B: some insights into the structural basis of its stability and substrate specificity."; Proteins 51:489-497(203).
                                                                                                                                                                                                                                                                                                                                                                                                                          174 IVGYSNAQGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS). PubMed=12784208; DOI=10.1002/prot.10319; Biswas S., Chakrabarti C., Kundu S., Jagannadham M.V., Dattagupta J.K.;
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NCBI_TaxID=94328;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thiol protease.
ACT_SITE 27
ACT_SITE 161
DISULFID 24
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P82474;
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                                                                                                                                                            70 GCHGDTIPRGIEYIQHNGVVQ-ESYYRYVAREQSCRRPNAQRFGISNYCQIYPPNANKIR 128
                                                                                                                                                                                     62 GCNGGMMNNAFQYIITNGGIDTQQNYPYSAVQGSCKPYRLRVVSINGFQRVTRNNESALQ 121
                                                                                                                                                                                                                                           129 EALAQTHSAIAVIIGIKDLDA----FRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQGVD 184
                                                                                                                                                                                                                                                                                122 SAVASQPVSVTV-----EAAGAPFQHYSS-GIFTGPCGTAQN-HGVVIVGYGTQSGKN 172
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                                                                                 11 PAEIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDC-ASOH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21332182; PubMed=11438432; DOI=10.1016/S1383-5769(01)00068-X; Grams R., Vichasri-Grams S., Sobhon P., Upatham E.S., Viyanant V.; "Molecular cloning and characterization of cathepsin L encoding genes
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fasciola gigantica (Giant liver fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Echinostomida; Echinostomata; Fascioloidea; Fasciolidae; Fasciola.
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                                         22;
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G0; G0:0004197; F:cysteine-type endopeptidase activity; IEA.
G0; G0:0004197; F:cysteine-type and peptidolysis; IEA.
G0; G0:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000668; Peptidase C1.
InterPro; IPR000169; Pept cys acsite.
Pfam; PF00112; Peptidase C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grams S.V., Grams R., Sobhon P., Viyanant V., Upatham E.S., Submitted (FEB-2000) to the EWBL/GenBank/DDBJ databases. - SIMILARITY: Belongs to peptidase family Cl. EMBL, AF239267, AF444678.1; -. HSSP; PS3634; 1K3B.
Query Match 26.1%; Score 315; DB 1; Length 215; Best Local Similarity 34.5%; Pred. No. 3.7e-20; Matches 76; Conservative 32; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 AA; 24217 MW; 7F443104B4071D3C CRC64;
                                                                                                                                                                                                                                                                                                                        YWIVRNSWDTNWGDNGYGYFAANI-----DLMMIBEYP 217
                                                                                                                                                                                                                                                                                                                                                             173 YWIVRNSWGQNWGNQGYIWMERNVASSAGLCGIAQLPSYP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 AA
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SMART; SM00645; Pept Cl; 1.
PROSITE; PS00640; THIOL PROTEASE ASN; 1.
PROSITE; PS00639; THIOL PROTEASE TYS; 1.
PROSITE; PS00639; THIOL PROTEASE TYS; 1.
Hydrolase; Protease; Thiol protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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Parasitol. Int. 50:105-114(2001).
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Matches 73; Conservative
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62 NYGCMGGLMENAYEYLKQFGLETESSYPYTAVEDQCR--YNRQLGVAKVTDYYTVHSGSE 119
                                                                                                120 VELKNLVGAEGPAAVAV----DVESDFMMYSGGIYQSRTCSSLRVNHAVLAVGYGTQGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukāryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Zingiberales, Zingiberaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Choi K.H., Laursen R.A.;
"Amino-acid sequence and glycan structures of cysteine proteases with
proline specificity from ginger rhizome Zingiber officinale.";
Bur. J. Biochem. 267:1516-1526(2000).
-!- CATALYTIC ACTIVITY: Preferential cleavage with a proline residue
                                                                    125 NKIREAL-AQTHSAIAVIIGIKDLDA-FRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct protein sequencing; Glycoprotein; Hydrolase;
                                                                                                                                                                                   183 VDYWIVRNSWDTNWGDNGYGYFAAN------IDLAMIEEYP
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N-linked (GlcNAc. .).
/FTId=CAR_000200.
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Prodom; PD000158; Peptidase_C1; 1.

SMART; SM00645; Pept_C1; 1.

PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG-PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.

PROSITE; PS00639; THIOL_PROTEASE_CYS; 1.
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By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlcNAC...
                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
25-octraproteinase GP-II (EC 3.4.22.-).
Zingiber officinale (Ginger).
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InterPro; IPR000169; Pept cys acsite.
InterPro; IPR000668; PeptIdase_C1.
Pfam; PF00112; Peptidase_C1; 1.
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MEDLINE=20156257; PubMed=10691991;
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PDB; 1CQD; X-ray; A/B/C/D=1-221.
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161
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InterPro; IPR000169; Pept_cys_acsite.
InterPro; IPR000668; Peptidase_C1.
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ProDom; PD000158; Peptidase C1; 1.

SMART; SM00645; Pept C1; 1.
                                                                TISSUE=Liver;
MEDLINE=88050863; Pubmed=3676277
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177 218
25 25
165 165
165 109
72 65
6 99
72 99
8 207
8 207
109 N
197 Mi
                 TEBS Lett. 209:330-334(1986)
   chicken liver cathepsin L.";
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tes 70; Conserv
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                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCRGGWMNPAPQFIVNNGGINSEETYPYRGQDGICNSTVNAPVVSIDSYENVPSHNEQSL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REALAQTHSAIAVIIGIKDLDAFRH--YDGRTIIQRDNGYQPNYHAVNIVGYSNAQGVDY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 PAEIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDC-ASQH
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87080783; PubMed=3792553; DOI=10.1016/0014-5793(86)81137-1; Wada K., Tanabe T.; "N-terminal amino acid sequences of the heavy and light chains of
                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                25.8%; Score 311; DB 1; Length 221; 33.8%; Pred. No. 8.8e-20; ive 34; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                    23922 MW; 909A312BD8632D42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wada K., Takai T., Tanabe T.;
"Amino acid sequence of chicken liver cathepsin L.";
Eur. J. Biochem. 167:13-18(1987).
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01-MAR-1989 (Rel. 10, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Cathepsin L (EC 3.4.22.15) (Fragments).
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WIVKNSWGKNWGESGYIRAERNIE 200
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213
221 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P09648;
01-MAR-1989
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ID CATL CH
DT O1-MAR.
DT 01-MAR.
DT 25-0CT.
DB CATHORN
GN GAILUS
OC BUKATY.
OC Archos.
OC Archos.
OC Archos.
CO GAILUS
CO GAI
                                                                                                                                                                                                                                                                                         STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus
                                                                        HEL I X
TURN
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124 ANKIREALAQTHS-AIAVIIGIKOLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQG 182 67 SQHGCHGDTIPRGIEYIQHN-GVVQESYYRYVAR-EQSCR-RPNAQRFGISNYCQIYPPN 123 99 "Purification and amino acid sequence of chicken liver cathepsin L."; Biochemistry 26:5689-5695(1987). 10 APAEIDLROMRIVIPIRMOGGCGSCWARSGVAATESAYLAHRNOSLDLAEQELVDCA--compared to cathepsin B, cathepsin L exhibits higher activity cowards protein substrates, but has little activity on Z-Arg-Arg-NHMec, and no peptidyl-dipeptidase activity.

SUBUNIT: Dimer of a heavy and a light chain linked by disulfide 14; Gaps lysosomes.
-!- CATALYTIC ACTIVITY: Specificity close to that of papain. As PROSITE; PS00640; THIOL PROTEASE ASN; 1.
PROSITE; PS00139; THIOL PROTEASE CYS; 1.
PROSITE; PS00639; THIOL PROTEASE HIS; 1.
Direct protein sequencing; Glycoprotein; Hydrolase; Lysosome; Jufour E., Obled A., Valin C., Bechet D., Ribadeau-Dumas B., DB 1; Length 218; By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAC. ..).
By similarity.
Interchain (By similarity).
Q -> I (in Ref. 3).
S -> N (in Ref. 3).
RTK -> FKT (in Ref. 3).
Nissing (in Ref. 3).
N -> K (in Ref. 3).
N -> K (in Ref. 3).
I -> Q (in Ref. 3). 24.9%; Score 300; DB 1; Length 21 31.7%; Pred. No. 8.46-19; ive 37; Mismatches 100; Indels 183 VDYWIVRNSWDTNWGDNGYGYFAA----NIDLMMIEEYPYV 219 KKYWIVKNSWGEKWGDKGYIYMAKDRKNHCGIATAASYPLV 218 Cathepsin L heavy chain. Cathepsin L light chain -1- SUBCELLULAR LOCATION: Lysosomal.

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63 CKGGWVNRAYDFIISNNGVTTDENYPYRAYQGTC---NANYFPNSAYITGYSYVRRNDES 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNA
                                                                                                                                                                                                                                                                                                                                                                           221 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000169; Pept cys acsite.
InterPro; IPR000668; Peptidase_C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20156257; PubMed=10691991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 2
24241 MW;
                                                                                                                                                                        188 VRNSWDTNWGDNGY 201
                                                                                                                                                                                                         ||||| ::|| ||
174 VRNSWGSSWGQGGY 187
                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR, A59040; A59040.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=94328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; C01.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct protein
ACT SITE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P82474;
                                                                                                                                                                                                                                                                                                                                                                           GPI ZINOF
P82473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
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DISÜLFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                                                                                             GPI_ZINOF
                                                                                                                                                                                                                                                                                                                                                                                                      DDT TO DD TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQSIDWRDYGAVGEVKNQGPCGGGWAFAAIATVBGIYKIRKGNLVYLSEQEVLDCAVSYG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAEIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEOELVDCASOHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20153315; PubMed=10686143; DOI=10.1006/prep.1999.1165; Lopez L.M.I., Sequeiros C., Natalucci C.L., Brullo A., Maras B., Barra D., Caffini N.O.; "Purification and characterization of macrodontain I, a cysteine Purification en characterization of peptidase from unripe fruits of Pseudananas macrodontes (Morr.) Harms (Bromeliaceae).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein Expr. Purif. 18:133-140(2000).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Ala-|-Xaa > Gln-|-Xaa Tyr-Xaa >> Leu-|-Xaa > Gly-|-Xaa.
-!- ENZYME REGULATION: Inhibited by E-64 (L-trans-epoxysuccinyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete sequence and kinetic aspects of macrodontain I, a cysteine endopeptidase of Pseudananas macrodontes.";
                                                                                                                                                                                    Prededananas macrodontes (Pseudananas sagenarius).
Bukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Bromeliaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-27, CATALYTIC ACTIVITY, ENZYME REGULATION, SUBUNIT, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: Fruits.
-!- MASS SPECTROMETRY: MW=23458.63; METHOD=MALDI; RANGE=1-213;
NOTE=Ref.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity; IDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.5%; Score 295; DB 1; Length 213; 35.1%; Pred. No. 2.3e-18; ive 30; Mismatches 84; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                           Natalucci C.L., Lopez L.M.I., Brullo A., Maras B., Turk B., Caffini N.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEB76E632EA77026 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00645; Pept Cl, 1.
PROSITE; PS00640; THIOL PROTEASE ASN; 1.
PROSITE; PS00139; THIOL PROTEASE CYS; 1.
PROSITE; PS00639; THIOL PROTEASE HIS; 1.
Direct protein sequencing; Hydrolase; Thiol protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P14080; IYAL.

MEROPS; CO1.028; -

Oc. GO:0004197; F:cysteine-type endopeptidase activi
GO; GO:0005508; P:proteolysis and peptidolysis; IDA.

InterPro; IPR000169; Pept cys acsite.

InterPro; IPR000668; Peptidase_C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- MISCELLANEOUS: The optimum pH is 6.1-8.5.
                                                                           (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
                           213 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leucylamide-(4-guanido)-butane).
SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-2002) to Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00705; PAPAIN. ProDom; PD000158; Peptidase_C1; 1.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00112; Peptidase_C1; 1.
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                                                                                                                                                                     Macrodontain I (EC 3.4.22.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68; Conservative
                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                  NCBI TaxID=203992;
                                                                                                                                          (Rel
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fruit,
                                                                                 28-FEB-2003
                                                                                                            28-FEB-2003
                                                                                                                                          25-OCT-2004
                                                                                                                                                                                                                                                                                       Pseudananas
                        MDO1 PSEMR
P83443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAEIDLROMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDCASQ-H 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Cysteine proteinse (BP-I (EC 3.4.22.-).
Zingiber officinale (Ginger).
Subaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Zingiberaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choi K.H., Laursen R.A., "Amino-acid sequence and glycan structures of cysteine proteases with proline specificity from ginger rhizome Zingiber officinale."; Eur. J. Biochem. 267:1516-1526(2000)
128 REALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQGVDYWI
                                              PDSIDWREKGAVVPVKNQGGCGSCWAFDAIAAVEGINQIVTGDLISLSEQQLVDCSTRNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Match 24.5%; Score 295; DB 1; Length 221;
Local Similarity 32.0%; Pred. No. 2.4e-18;
Les 65; Conservative 35; Mismatches 91; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PREMIX PRODUIT; Peptidaec C1; 1.
PRINTS; PROO15; PapalN.
PRODOM; PD000158; Peptidaec C1; 1.
PROSTR; S000645; Pept C1; 1.
PROSTR; PS00640; THIOL, PROTEASE ASN; 1.
PROSTR; PS00639; THIOL_PROTEASE CYS; PALSE NEG.
PROSTR; PS00639; THIOL_PROTEASE HIS; PALSE NEG.
Direct protein_sequencing; Glycoprotein; Hydrolase; Thiol protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
V or D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the peptidase C1 family.
-!- CAUTION: The authors regard the sequence as tentative, as t
believe that it may have been contaminated by a homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3035D7870EA743DB CRC64;
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| Tabernaemontana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissum=Latex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rissum=Latex;
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     THE FET THE REAL PROPERTY OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
REALAQTHSAIAVIIGIKDLDAFRH--YDGRTIIQRDNGYQPNYHAVNIVGYSNAQGVDY 185
                                         CHGDTIPRGIEYIQHN-GVVQESYYRYVAREQSCRRPNAQRFGISN-YCQIYPPNANKIR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNGGLMDLAFEYIKDNHGIDTEESYPYVGRDMKCHFKKKDIGAVDNGYVDLPEGDEEALK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EALA-QTHSAIAVIIGIKDLDAFR---HYDGRTIIQRDNGYQPNYHAVNIVGY-SNAQGV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 IDLRQMRTVTFIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQELVDCASQ---HG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VDWRDKGLVTEVRNOGMCGSCWAFSATGALEGQHARASGGMVSLSEQNLVDCSTKYGNHG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Britton C., Murray L.;

A cathepsin L procease essential for Caenorhabditis elegans

"A cathepsin L procease essential for Caenorhabditis elegans

"E murryogenesis is functionally conserved in parasitic nematodes.";

Mol. Biochem. Parasitol. 122:21-33(2002).

"E MEL, AP320084, AAL37181.1;

"E MEL, AP320084, AAL37181.1;

"M RSSP; PO7711; 1CJL.

"M RSSP; PO7711; 1CJL.

"M RSSP; PO7711; 1CJL.

"M RSSP; PO7711; 1CJL.

"M ROPS; C01.066; --

"GO; GO:0006508; P:proteclype endopeptidase activity; IEA.

"GO; GO:0006508; P:proteclysis and peptidolysis; IEA.

"GO; GO:0006508; P:proteclysis and peptidolysis; IEA.

"GO; GO:0006508; P:proteclysis and peptidolysis; IEA.

"R PROSITE; PRO0103; Pept C1; 1.

"M RNRY: SM00645; Pept C1; 1.

"M RNRY: SM00649; THIOL_PROTEASE_CN; 1.

"M Hydrolase; Protease; Thiol_PROTEASE_HIS; 1.

"M "MATCHARSE CNS."

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=22072558; PubMed=12076767; DOI=10.1016/S0166-6851(02)00066-X;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Nemātoda, Chromadorea, Rhabditida, Strongylida,
Ancylostomatoidea, Ancylostomatidae, Ancylostomatinae, Ancylostoma.
NCBI_TaxID=29170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 AA; 23486 MW; 4A339A1A7A61E525 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 20, Last sequence update) (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                214 AA
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(Rel. 44, Last sequence update)
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DYWLVKNSWGTGWGEKGYIRIARN 198
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WIVKNSWGKNWGESGYIRVERNI 199
                                                                                                               WIVENSWDTNWGDNGYGYFAANI 208
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01-WAR-2002 (TrEMBLrel. 20, Last seq
01-WAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cathepsin L-like protease (Fragment)
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ID ERVC_TABDI
AC P83654;
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DT 05-JUL-2004 (
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Procession of (EC 34.22.) (ERV-C)

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Substructed divisitates (Creps) statistical (Ervatamia coronaria).

Substruction and divisitate (Creps) statistical (Ervatamia coronaria).

Substruction and divisitate (Creps) statistical (Ervatamia coronaria).

Substruction and divisitates (Erratopopyta; Embryophyta; Trachoophyta; Trac
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                                                                                                                                                               GCHGDTIPRGIEYIQHNGVVQ-ESYYRYVAREQSCRRPNAQRFGISNYCQIYPPNANKIR 128
                                                                                                                                                                                                              EALAQTHSAIAVIIGIKDLDA----FRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAOGVD 184
                                                                                                                                                                                                                                      121 QAVAVQPSTVAI-----DASSAQFQQYSS-GIFSGPCGTKLN-HGVTIVGYQ----AN 167
                                                                                                                                        61
                                                                                                              11 PAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQELVDC-ASQH 69
                                                                                                                                      PEQIDWRKKGAVTPVKNQGSCGSCWAFSTVSTVESINQIRTGNLISLSEQELVDCDKKNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Spleen;
MEDLINE-9125734; PubMed=2044774; DOI=10.1016/0014-5793(91)80620-1;
Ritonja A., Colic A., Dolenc I., Ogrinc T., Podobnik M., Turk V.;
The complete amino acid sequence of bovine cathepsin S and a partial sequence of bovine cathepsin L.";
FEBS Lett. 283:329-331(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The specificity of bovine spleen cathepsin S. A comparison with rat liver cathepsins L and B."; Blochem. J. 264:475-481(1989).
-1- FUNCTION: Thiol protease. The bond-specificity of this proteinase.
                                                                                        Gaps
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MEDLINE-91323515; PubMed=1864368; DOI=10.1016/0014-5793(91)80971-5;
Mederanders B., Broemme D., Kirschke H., Kalkkinen N., Rinne A.,
Paquette T., Toothman P.;
"Primary structure of bovine cathepsin S. Comparison to cathepsins
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Spleen;
MEDLINE=92384944; PubMed=1515067;
MEDLINE=92384946; PubMed=1515067;
Dolenc I., Ritonja A., Colic A., Podobnik M., Ogrinc T., Turk V.;
Bovine cathepsins S and L: isolation and amino acid sequences.";
Biol. Chem. Hoppe-Seyler 373:407-412(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
MEDLINE-90104320; PubMed-2604727;
Broemme D., Steinert A., Friebe S., Fittkau S., Wiederanders B.,
                                                                                        20;
                                                              23.7%; Score 286; DB 1; Length 208; 36.5%; Pred. No. 1.4e-17;
                                                                                      78; Indels
  196 K -> W (in Ref. 3).
21 S -> W (in Ref. 3).
22521 MW; 13CD944089802C12 CRC64;
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01-MAY-1992 (Rel. 22, Last sequence update)
02-COT-2004 (Rel. 45, Last annotation update)
Cathepsin S (EC 3.4.22.27).
                                                                                                                                                                                                                                                                                                                                                     217 AA
                                                                                     27; Mismatches
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FEBS Lett. 286:189-192(1991).
                                                                                     72; Conservative
                                                                                                                                                                                                                                                                                                                                                      STANDARD;
 151
17
21
208 AA;
                                                                           Local Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                              cathepsin N. CATALYITY: Similar to cathepsin L, but with much less activity on Z-Phe-Arg-|-NHMec, and more activity on the Z-Val-Val-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 PAEIDLROMRIVIPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDCAS---
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R InterPro; IPR00069; Peptidase_C1.
Pfam: PF00112; Peptidase_C1; 1.
R PRINTS; PR0705; PAPAIN.
R PRNTS; PR0705; Peptidase_C1; 1.
R PRNSTP; SM00645; Peptidase_C1; 1.
R PROSTTE; PS00640; THIOL_PROTEASE ASN; 1.
R PROSTTE; PS00640; THIOL_PROTEASE CYS; 1.
T ACT SITE 25 150 110 By similarity.
T ACT SITE 184 184 By similarity.
T DISULPID 12 110 By similarity.
T DISULPID 56 99 By similarity.
part similar to the specificities of cathepsin L and
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D180A37E8CD07F45 CRC64;
                                                                                                                             Arg-|-Xaa compound.
-!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Lysosomal.
-!- SIMILARITY: Belongs to the peptidase C1 family.
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Best Local Similarity 33.8%; Pred. No. 2.1e-17;
Matches 69; Conservative 33; Mismatches 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 DYWLVKNSWGLHFGDQGYIRMARN 201
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164
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217 AA;
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5.1.6
Compugen Ltd.
version 5
GenCore (c) 1993
        Copyright
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protein search, using sw model OM protein - Run on:

May 19, 2005, 17:32:37; Search time 161 Seconds (without alignments) 533.297 Million cell updates/sec

US-09-867-159A-2 1206 Title: Perfect score:

1 TWACSINGNAPAEIDLRQMR......YFAANIDLMMIEEYPYVVIL 222

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 segs, 386760381 residues Searched:

1481396 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 222 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_16Deco4:*
1: geneseqp1980s:*
2: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2003bs:* geneseqp2001s: geneseqp2002s: geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	цо	Cysteine	Cysteine	House dus	D. pteron	House dus	House dus	Der p1 al	Dust mite	House dus	Protein a	House dus	Ноиве див	House dus	House dus	House dus	House dus	House dus	House dus	_		Euroglyph	House dus	House dus	Euroglyph	Euroglyph
	Description	Aao20568	Abb98533	Aau07748	Aab98347	Aau07746	Abg67023	Adk52140	Adr87225	Aau07747	Aar52742	Abg67024	Abg67030	Abg67027	Abg67029	Abg67026	Abg67028	Abg67025	Abg67032	Abg67031	Aay25678	Adc34926	Abg67034	Abg67033	Aay25677	Aay25676
SUMMAKIES	ID	AA020568	ABB98533	AAU07748	AAB98347	AAU07746	ABG67023	ADK52140	ADR87225	AAU07747	AAR52742	ABG67024	ABG67030	ABG67027	ABG67029	ABG67026	ABG67028	ABG67025	ABG67032	ABG67031	AAY25678	ADC34926	ABG67034	ABG67033	AAY25677	AAY25676
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ALIGNMENTS

Antiallergic, antiinflammatory; antiasthmatic; dermatological; allergen; anti-histamine; histamine synthesis inhibitor; allergic hypersensitivity; allergic asthma; allergic rhinitis; cysteine protease protein; enzyme; AAO20568 standard; protein; 222 AA (first entry) Cysteine protease protein. atopical eczema. 02-JAN-2003 RESULT 1

Dermatophagoides pteronyssinus.

/note= "Encoded by ACC" Location/Qualifiers Misc-difference 105 WO200278736-A2

10-OCT-2002.

30-MAR-2001; 2001FR-00004370. 03-MAY-2001; 2001FR-00005929. 29-MAY-2001; 2001US-00867159. 28-MAR-2002; 2002WO-FR001098.

(ANTI-) ANTIALIS SARL.

Trehin Y; Terrasse G, Loria E,

WPI; 2002-750636/81. N-PSDB; AAL41281.

Antiallergic compositions containing an anti-histamine, a histamine synthesis inhibitor, and optionally an allergen or nucleic acid coding

Claim 13; Page 30-31; 32pp; French.

for the allergen.

The invention relates to antiallergic compositions containing an anti-histamine, a histamine synthesis inhibitor, and optionally an allergen or isolated nucleic acid molecule that has at least one polymucleotide sequence coding for the allergen, together with a pharmaceutical carrier.

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Sequence 222
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hes 222;
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14-APR-1993;
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                                                                                                                         Gaps
          specific antiallergic treatment, and also useful in the treatment of allergic hypersensitivity, allergic asthma, allergic and allergic and allergic and atopical eczema. This sequence represents the cysteine protesin relating to the antiallergic compositions of the
  the invention is useful as a non-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antiallergic; antiasthmatic; antiinflammatory; dermatological;
                                                                                                 100.0%; Score 1206; DB 5; Length 222; 100.0%; Pred. No. 2.7e-127; ive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunotherapy, allergen, allergic hypersensitivity reaction, allergic asthma; allergic rhinitis, allergic atopic eczema; cysteine protease.
                                                                                                                                                                                                                                                                                             QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antiallergic composition, useful for preventing rhinitis or eczema, containing at least two of a and histamine synthesis inhibitor.
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composition of
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                                                                                                           Local Similarity
les 222; Conserv
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                                                                          Sequence 222 AA;
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The present invention relates to an antiallergic pharmaceutical

Claim 7; Page 27-28; 33pp; French

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composition (I) comprising a pharmaceutical carrier containing an active agent combination of at least two of; an allergen; an antihistemaine; and a histamine synthesis inhibitor. (I) is used for treating or preventing allergic hypersensitivity reactions, especially allergic asthma, allergic rhintis or allergic toppic eczema, in babies, children or adults. The present sequence is cysteine protease from Dermatophagoides pteronyssinus, which was used as an allergen in the invention
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Dermatophagoides (house dust mites), useful for treating house dust m
allergy in humans, and for diagnosing sensitivity to house dust mite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               House dust mite; allergenic protein; Der p I; Der p II; Der f I; Der f II; antiallergenic; immunostimulant; house dust mite allergy; T-cell epitope; polymorphic variant.
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100.0%; Pred. No. 2.7e-127;
tive 0; Mismatches 0;
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92US-00881396.
93WO-US003471.
94US-00227772.
95US-00445307.
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Shaked Z;
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N-PSDB; AAH22385.
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                                        The invention relates to an isolated peptide of the major protein

allergens of the genus Dermatophagoides, which comprises at least one T

call group of a protein allergen from Der p (DP) I, Der f (DF) I

cor DF II. The isolated peptide comprises at least two regions, each

region comprising at least one T cell group of a protein allergen of the

genus Dermatophagoides. The regions are derived from the same or

different protein allergens of the genus Dermatophagoides. The peptides

are useful for treating house dust mite allergy in humans. The peptides

are also useful for detecting or diagnosing sensitivity to house dust

mite protein allergens. The present peptides have similar or enhanced

therapeutic properties as the naturally-occurring allergen, but have

creduced side effects, and increased solubility and stability. The present

sequence represents an allergenic protein from Dermatophagoides from

which the T-cell epitope containing peptides are derived, a polymorphic

variant of Der p I. Note: The present sequence is not shown in the

specification but is derived from the Der p I sequence shown in figure 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mite group 1 protein; methyltrophic yeast; Escherichia coli; allergy; recombinant mite group 1 protein; allergic response; antiallergic; infectious disease; allergic disease.
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                                                                                                                                                                                                                                                                                 Length 222;
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99.5%; Pred. No. 5.8e-127;
ive 1; Mismatches 0;
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                        Disclosure; Fig 22; 158pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB98347 standard; protein; 222
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                                                                                                                                                                                                                                                                                                        221; Conservative
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                                                                                                                                                                                                                                                                                              Local Similarity
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 protein allergens
                                                                                                                                                                                                                                                         Sequence 222 AA;
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The present invention describes a method for the production of a recombinant mite Group 1 protein (I). The method comprises culturing a methyltrophic yeast microorganism transformed with a nucleic acid molecule (II) encoding (I), and recovering (I), or culturing Escherichia coli transformed with (II) under conditions in which (I) forms an inclusion body in E. coli, isolating the inclusion body, and recovering (I). Also described is a method for detecting mite allergy in an animal comprising: (a) contacting (I) with a putative igE-containing substance to form a complex between (I) and IgE; and (b) determining the presence of reactive with (I) by detecting the complex, where the presence of reactive igE is indicative of mite allergy in the animal. (I) is useful for detecting mite allergy in an animal, or in a composition to reduce allergic response to a mite Group I protein in a mite allergic animal.

(I) is also useful in a composition for treating or preventing allergic, infectious or other diseases. AAH22336 to AAH22394 and AAB98136 to AAB98149 represent sequences used in the exemplification of the present
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Producing recombinant mite Group 1 protein for treating allergies, involves culturing a methyltrophic yeast microorganism or Escherichia coli transformed with nucleic acid molecule, and recovering the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 99.5%; Score 1200; DB 4; Length 222; Local Similarity 99.5%; Pred. No. 1.3e-126; nes 221; Conservative 1; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild-type Ala substituted by Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild-type His substituted by Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGVDYWIVRNSWDTNWGDNGYGYFAANIDLAMIEEYPYVVIL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 House dust mite allergenic protein Der p I variant b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-cell epitope; polymorphic variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                          Claim 12; Page 145; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU07746 standard; protein; 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dermatophagoides pteronyssinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6268491-B1
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The invention relates to an isolated peptide of the major protein allergens of the genus Dermatophagoides, which comprises at least one T cell group of a protein allergen from Der D (DP) I, DP II, Der f (DP) I or DF II. The isolated peptide comprises at least two regions, each region comprising at least one T cell group of a protein allergen of the genus Dermatophagoides. The regions are derived from the same or different protein allergens of the genus Dermatophagoides. The regions are derived from the same or care useful for treating house dust mite allergy in humans. The peptides are useful for detecting or diagnosing sensitivity to house dust interapeutic properties as the naturally-occurring allergen, but have reduced side effects, and increased solubility and stability. The present sequence represents an allergenic protein from Dermatophagoides from which the T-cell epitope containing peptides are derived, a polymorphic variant of Der p I. Note: The present sequence is not shown in the specification but is derived from the Der p I sequence shown in figure 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptides comprising T cell groups of the major allergens from Dermatophagoides (house dust mites), useful for treating house dust mite allergy in humans, and for diagnosing sensitivity to house dust mite protein allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                   Chen X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Rogers BL, Franzen HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
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                                                                                                                                                                                                                                                                                                                                                                                                                   Greenstein JL, Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 22; 158pp; English.
                                                                                                                              91US-00777859.
92US-00881396.
93WO-US003471.
94US-00227772.
95US-00445307.
                                                                95US-00484296
                                                                                                                                                                                                                                                                                                                                               (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 99.1
les 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Shaked Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-549074/61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 222 AA;
                                                                                                                                                                                                                                          14-APR-1994;
19-MAY-1995;
                                                                07-JUN-1995;
                                                                                                                                     16-OCT-1991;
                                                                                                                                                                         38-MAY-1992
                                                                                                                                                                                                      14-APR-1993
31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                   Garman RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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The invention relates to a recombinant allergen (I) which is a mutant of a naturally occurring allergen, where the mutant allergen has at least C four primary mutations, which each reduce the specific immunoglobulin E (10g) binding capability of the mutated allergen as compared to the IgE binding capability of the naturally occurring allergen, where each primary mutation is a substitution of one surface-exposed amino acid cresidue with another residue, which does not occur in the same position in the amino acid sequence of any known homologous protein within the taxonomic species from which the naturally occurring allergen originates, and each primary mutation is spaced from each other primary mutation by at least 15 Angstrom and the primary mutations are placed in such a manner that at least one circular surface region with a area of 800 comprising two or more of the recombinant allergens, where they variant comprising two or more of the recombinant allergens, where the variant capsent in at least one of the other variants, and for each variant not secondary mutation; a DNA sequence encoding the recombinant allergen from each absent in at least one of the other variants, and for each variant not secondary mutation; a DNA sequence encoding the recombinant allergen confidence which hybridises to it under stringent confittons, where the sequence encodes a peptide having at least one B cell epitope; and experime of the recombinant allergen is useful as a pharmaceutical for preparing and pharmaceutical for preventing and/or treating allergy, or in expression vector comprising the DNA and a host cell comprising the comprising and assessed for the level of reactivity between the recombinant allergen and assessed for the level of reactivity between the recombinant allergen and assessed for the level of for the recombinant allergen or treatment of a subject, or for vectorizing or treatment of a subject or for the recombinant proversion or resonance or preparion or preparion or treatment of a subject or sequence or ever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reatment, prevention or alleviation of allergic reactions in a subject a.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic anaphylaxis. The present sequence represents a wild-type allergen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 60
                   Immunoglobulin E; 19E; allergen; allergy; hay fever; rhinoconductivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or preventing and/or treat reduced immunoglobulin E
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                                       rhinitis, asthma, systemic anaphylaxis, vaccine, antiallergic, B cell epitope.
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Pred. No. 3.6e-126;
1; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                            Spangfort MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant mutant allergen, useful for allergy, comprises multiple mutations and re
                                                                                                                                                                                                                                                                                                                                                                                                                                              Holm J, Ipsen H, Nedergaard Larsen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Page 103-104; 210pp; English
                                                                                                              Dermatophagoides pteronyssinus
                                                                                                                                                                                                                                                                                              16-NOV-2000; 2000DK-00001718.
16-NOV-2000; 2000US-0249361P.
14-JUN-2001; 2001US-0298170P.
                                                                                                                                                                                                                                                       16-NOV-2001; 2001WO-DK000764
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Best Local Similarity 99.1%;
Matches 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                (ALKA-) ALK-ABELLO AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding affinity.
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ABG67023 standard; protein; 222 AA

RESULT

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요 ò 셤 House dust mite allergen Der p 1.

(first entry)

24-SEP-2002

ABG67023;

ABG67023 ID ABG(XX AC ABG XX DT 24-XX DE HOU

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121 PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY
                                                                                                                                                                                      QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                                                                                             ADR87225 standard; protein; 222
                                                                                                                                                                                                                                                                                                                                                                                                                     16-DEC-2004
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ADR87225
LD ADR8 7225

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method for production of a recombinant protein allergen from an acarid of the genera Dermatophagoides or Buroglyphus. The allergens and also antibodies raised against them, are useful for diagnosis and treatment of allergies to house dust mites. When expressed in plants, allergens are synthesized and matured to biologically active form, with essentially the same pattern of glycosylation as the native protein. Recombinant expression provides a pure protein; contrast complex mixtures of allergens currently used. The present sequence represents Der pl allergen.
                                                                                                                                                                       PPNVNKIREALAQTHSAIAVIIGIKOLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                               PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant production of acarid protein allergen, useful for diagnosis and treatment of allergy to house dust mites, comprises growing transformed eukaryotes, particularly plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recombinant protein allergen; Antiallergic; Desensitization; antibody; allergy; house dust mite; allergen.
Dorlhac De Borne F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 222;
                                                                                                                                                                                                                                                      OGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
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Pred. No. 3.6e-126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STALLERGENES SA. SOC NAT EXPL IND TABACS & ALLUMETTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; SEQ ID NO 2; 55pp; French.
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                                                                                                                                                                                                                                                                                                                                                                          ADK52140 standard; protein; 222
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99.1%;
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rent A, Faye L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
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                                                                                                                                               121
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The invention relates to novel compositions including contiguous coverlapping peptide fragments which together form an entire amino acid sequence of an allergen, where the fragments are capable of inducing a T-cell response in patients who are hypersensitive to the allergen. The contiguous overlapping peptide fragments further result in lower levels of IgE stimulation activity. The lower levels of IgE stimulation activity. The lower levels of IgE stimulation activity are zero or weak. The contiguous overlapping peptide fragments further result in a decrease in T-cell response upon subsequent exposure to the allergen, thus, modulating an immune response in the patients, who are hypersensitive to the allergen. A composition of the invention has a cariallergic activity, and may have a use in gene therapy, and as a vaccine. The composition and methods are useful for preventing or treating IgE-mediated allergies. The present sequence represents an allergen of the invention, dust mite Der pl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New compositions including contiguous overlapping peptide fragments that form an entire amino acid sequence of an allergen (e.g. bee venom or birch pollen allergen), useful for preventing or treating IgE-mediated
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                                                                                                                                                                     dust mite; allergen; Der p 1; T-cell response; IgE; immunoglobulin E; immune response; antiallergic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                     Dust mite allergen Der p 1 SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 14; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2003; 2003US-0455004P.
12-MAR-2004; 2004US-00799514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-2004; 2004WO-IB001300
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.1<sup>1</sup>
Matches 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYLA-) UNIV LAUSANNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-668931/65.
                                                                                                                                                                                                                                                                                                       Dermatophagoides sp
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                                                                                                                                                                                                                                                                                                                                                                                       WO2004081028-A2
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Gaps

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Best Local Similarity >>... Matches 220; Conservative

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TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 60 ö

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Length 222; Indels 9 9 120 120

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different protein allergens of the genus Dermatophagoides. The peptides are useful for treating house dust mite allergy in humans. The peptides are useful for treating house dust mite allergy in humans. The peptides are also useful for detecting or diagnosing sensitivity to house dust mite protein allergens. The present peptides have similar or enhanced therapeutic properties as the naturally-occurring allergen, but have reduced side effects, and increased solubility and stability. The present sequence represents an allergenic protein from Dermatophagoides from which the T-cell epitope containing peptides are derived, a polymorphic variant of Der p I. Note: The present sequence is not shown in the specification but is derived from the Der p I sequence shown in figure 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                  1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                          TNACSINGNAPAEIDLRQMRTVTPIRMQGGGSCWAFSGVAATESAYLAYRNQSLDLAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELVDCASQHGCHGDT1PRG1EY1QHNGVVQESYYRYVAREQSCRRPNAQRFG1SNYCQ1Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELVDCASQHGCHGDTI PRGIKYI QHNGVVQESYYRYVAREQSCRRPNAQRFGI SNYCQI Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                                                                                                                                                                                                         98.6%; Score 1189; DB 4; 98.2%; Pred. No. 2.2e-125; ive 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Ala or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= Ser or Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Der pI; House Dust Mite Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR52742 standard; protein; 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dermatophagoides pteronyssinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93WO-US008518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein allergen of Der pI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 98.2
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chua K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 81
                                                                                                                                                                                                                                                                                 Sequence 222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .0-SEP-1992;
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17-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-1994.
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                                                                         BLVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                  PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                          121 PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated peptide of the major protein allergens of the genus Dermatophagoides, which comprises at least one T cell group of a protein allergen from Der p (DP) I, DP II, Der f (DF) I or DF II. The isolated peptide comprises at least two regions, each region comprising at least one T cell group of a protein allergen of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mite
  Peptides comprising T cell groups of the major allergens from Dermatophagoides (house dust mites), useful for treating house dust mallergy in humans, and for diagnosing sensitivity to house dust mite protein allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Franzen HM, Chen X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              House dust mite, allergenic protein, Der p I; Der p II, Der f I; Der f II, antiallergenic; immunostimulant; house dust mite allergy; T-cell epitope; polymorphic variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ____/note= "Wild-type Glu substituted by Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Wild-type His substituted by Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild-type Glu substituted by Gln"
                                                                                                                                                                                                                                                    House dust mite allergenic protein Der p I variant c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Wild-type Ala substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Greenstein JL, Kuo M, Rogers BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 22, 158pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                AAU07747 standard; protein; 222
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92US-00881396.
93WO-US003471.
94US-00227772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shaked Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
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08-MAY-1992;
14-APR-1993;
14-APR-1994;
19-MAY-1995;
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                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU07747;
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                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
AAU07747
AAU0747
AAU0747
AAU0747
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AAU0747
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Thomas WR,

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Example 7; Page; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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ABG67030
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                                                                                                                                                                                                                                              ELVDCASQHGCHGDTIPRGIXY1QHNGVVQESYYRVVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                                      nseq
                                                                                                                                                                                                                                   ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                           PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                            AAR52742 is a mature Der pI mite allergen. The mature protein can be used to detect sensitivity in an individual to house dust mite and to reduce the sensitivity of the individual. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant mutant allergen, useful for preventing and/or treating allergy, comprises multiple mutations and reduced immunoglobulin E binding affinity.
                                                                                                                                                                                                       1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAXRNQSLDLAEO
                                                                                                                                                                                          1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin B; IgB; allergen; allergy; mutein; hay fever;
rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
vaccine; antiallergic; B cell epitope.
                             New protein allergens of house dust mite - used for diagnosing and treating sensitivity in an individual to house dust mite allergens.
                                                                                                                                                                        ..
0
                                                                                                                                                     Length 222;
                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                             QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEXYPYVVIL 222
                                                                                                                                                                                                                                                                                                                   QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIERYPYVVIL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spangfort MD;
                                                                                                                                                   Score 1177; DB 2;
Pred. No. 5.1e-124;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  House dust mite allergen Der p 1 mutant #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nedergaard Larsen J,
                                                                                                                                                                                                                                                                                                                                                                                        ABG67024 standard; protein; 222 AA
                                                          Disclosure; Fig 18; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dermatophagoides pteronyssinus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-NOV-2001; 2001WO-DK000764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-NOV-2000; 2000DK-00001718.
16-NOV-2000; 2000US-0249361P.
14-JUN-2001; 2001US-0298170P.
                                                                                                                                                   97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                       Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ALKA-) ALK-ABELLO AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-508328/54.
                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABK95640.
                                                                                                                                 Sequence 222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200240676-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                               24-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                            ABG67024;
                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
ABG67024
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The invention relates to a feeducing an entergent of a mutual to a naturally occurring alleagen, where the mutant alleagen has at least four primary mutations, which each reduce the specific immunoglobulin E (IgB) binding capability of the mutated alleagen as compared to the IgB binding capability of the mutaned alleagen as compared to the IgB chinding capability of the mutaning alleagen, where each primary mutation is a substitution of one surface-exposed amino acid residue with another residue, which does not occur in the same position of in the amino acid sequence of any known homologous protein within the taxonomic species from which the naturally occurring alleagen originates, and each primary mutation is spaced from each other primary mutation by at least one circular surface region with a area of 800 and secondary mutation is spaced from each other primary mutation by at least one circular surface region with a area of 800 comprises no mutation. Also included area composition comprising two or more of the recombinant allergens; where the valeant is at least one of the other variants, and for each variant no secondary mutation is present within a radius of 15 Angetrom from each absent primary mutation; a DNA sequence encoding the recombinant allergen cor its derivative, partial sequence or degenerated sequence, or a sequence which hybridises to it under stringent conditions, where the corpusing the DNA and a host cell comprising the C expression vector comprising the DNA and a host cell comprising the C vector. The recombinant allergen is useful as a pharmaceutical, for vector. The recombinant allergen is useful as a pharmaceutical, for the recombinant allergen and the recombinant allergen wineful for perventing an immune remarking and the recombina
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The invention relates to a recombinant allergen (I) which is a
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Best Local Similarity 96.8
Matches 215; Conservative
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Gaps

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Indels

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3; Mismatches

214; Conservative

Matches

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Sequence 222 AA;
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The invention relates to a recombinant allergen (I) which is a mutant of a naturally occurring allergen, where the mutant allergen has at least cour primary mutations, which each reduce the specific immunoglobulin E (19E) binding capability of the mutated allergen as compared to the IgE binding capability of the maturally occurring allergen, where each binding capability of the naturally occurring allergen, where each binding capability of the naturally occurring allergen, where each binding capability of the naturally occurring allergen, where each creation with another residue, which does not occur in the same position in the amino acid sequence of any known homologous protein within the caxonomic species from which the naturally occurring allergen originates, and each primary mutation is spaced from each other primary mutation by at least one circular sufface region with a area of 800 Angstrom ^2 comprises no circular sufface region with a area of 800 Angstrom of mutation. Also included are a composition comprising two or more of the recombinant allergens, where the variant not least one of the other variants, and for each variant not secondary mutation is present within a radius of 15 Angstrom from each obsent primary mutation; a DNA sequence encoding the recombinant allergen or its derivative, partial sequence or degenerated sequence or definitions, where the comprising the bunder stringent conditions, where the sequence encodes a peptide having at least one B cell epitope; and expression vector comprising the DNA and a host cell comprising the present in a harmanelial for preventing as pharmaceutical, for preventing as pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant mutant allergen, useful for preventing and/or treating allergy, comprises multiple mutations and reduced immunoglobulin E
                                             rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant; vaccine; antiallergic; B cell epitope.
Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spangfort MD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Page; 210pp; English.
                                                                                                                                                                                                                Dermatophagoides pteronyssinus
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16-NOV-2000; 2000US-0249361P.
14-JUN-2001; 2001US-0298170P.
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                                                                                                                                                                                                                                                                                                                                                                         WO200240676-A2
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Score 1162; DB 5; Length 222; Pred. No. 2.5e-122;

96.4%; 96.4%;

Best Local Similarity

Query Match

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120
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                                                                                                                                                                  61 ELVDCANQHGCHGDTIFRGIEYIQHNGVVQESYXRVVAQEQSCRRPNAQRFGISNYCQIY 120
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1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
                     1 TNACSINGNAPAEIDLRQMQTVTPIRMQGGGSCWAFSGVAATESAYLAVRNQSLDLAEQ
                                                                       61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY
                                                                                                                                                PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
vaccine; antiallergic; B cell epitope.
                                                                                                                                                                                                                        QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                                                                                                                         181 QGVDYMIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
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16-NOV-2000; 2000US-0249361P.
14-JUN-2001; 2001US-0298170P.
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                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                          ABG67027;
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                                                                                                                                                                                                                                                                                                                  RESULT 13
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allergen is defined by having at least one primary mutation, which is absent in at least one of the other variants, and for each variant no secondary mutation is present within a radius of 15 Ampstrom from each abent primary mutation; a DNA sequence encoding the recombinant allergen or its derivative, partial sequence or degenerated sequence, or a sequence which hybridises to it under stringent conditions, where the derivative, partial sequence, degenerated sequence or hybridising sequence encodes a peptide having at least one B cell epitope; an septence encodes a peptide having at least one B cell epitope; an cypression vector comprising the DNA and a host cell comprising the cypression vector. The recombinant allergen is useful as a pharmaceutical, for preparing a pharmaceutical for preventing and/or treating allergy, or in the recombinant allergen and assessed for the level of reactivity between the recombinant allergen and assessed for the level of reactivity between the IgE in the sample and the recombinant allergen and assessed for the level of reactivity between allergen or compositions are useful for generating an immune response in a subject, for vaccination or treatment of a subject or for the contractions are the recombinant encountered or the recombinant encountered or the recombinant encountered or a subject or for the contraction or allergen or a subject or set in a subject or the recombinant encountered enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic anaphylaxis. The present sequence represents a recombinant allergen of the invention. Note: The present sequence was not shown in the specification but was created by the indexer using information in the specification and the corresponding wild-type sequence
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ELVDCASQHGCHGDTIPEGIEYIQHNGVVQESYYRYVAEEQSCRRPNAQRFGISNYCQIY 120 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180 PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGQTIIQQDNGYQTNYHAVNIVGYSNA 180 TWACSINGWAPAEIDLRQMQTVTPIRMQGGCGSCWAFSGVAATESAYLAVRWQSLDLAEQ TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ ö 96.3%; Score 1161; DB 5; Length 222; 96.4%; Pred. No. 3.2e-122; ive 3; Mismatches 5; Indels (QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222 QGVDYMIVRNSWDTNWGDNGYGYFAANIDLAMIEEYPYVVIL 222 Best Local Similarity 96.4%; Matches 214; Conservative Sequence 222 AA; 61 19 121 181 181 Query Match 임 8 ద ઠે g ઠે 셤 ð

House dust mite allergen Der p 1 mutant #6. ABG67029 standard; protein; 222 (first entry) 24-SEP-2002 ABG67029; RESULT 14 ABG67029

Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever; rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant; vaccine; antiallergic; B cell epitope.

Dermatophagoides pteronyssinus. Synthetic.

WO200240676-A2.

16-NOV-2001; 2001WO-DK000764 23-MAY-2002.

16-NOV-2000; 2000DK-00001718. 16-NOV-2000; 2000US-0249361P. 14-JUN-2001; 2001US-0298170P.

(ALKA-) ALK-ABELLO AS

Spangfort MD; Ipsen H, Nedergaard Larsen J, Holm J,

WPI; 2002-508328 N-PSDB; ABK95645

nbinant mutant allergen, useful for preventing and/or treating comprises multiple mutations and reduced immunoglobulin \boldsymbol{E} recombinant mutant binding affinity.

Example 7; Page; 210pp; English.

The invention relates to a recombinant allergen (I) which is a mutant of a naturally occurring allergen, where the mutant allergen has at least (our primary mutations, which each reduce the specific immunoglobulin E (igg) binding capability of the mutated allergen as compared to the IgE binding capability of the mutated allergen, where each primary mutation is a substitution of one surface-exposed amino acid residue with another residue, which does not occur in the same position comparison of primary mutation is spaced from each other primary mutation by at least primary mutation is spaced from each other primary mutation by at least to manner that at least one circular surface region with a area of 800 and manner that at least one circular surface region with a area of 800 and manner that at least one circular surface region with a area of 800 and manner that a least one circular surface region with a area of 800 and position comprising two or more of the recombinant allergens, where the variant allergen is defined by having at least one primary mutation; and for each variant of secondary mutation is present within a radius of 15 Angstrom from each obsent in at least one of the other variants, and for each variant or sequence which hybridises to it under stringent conditions, where the sequence encodes a peptide having at least one B cell epitope; and expression vector comprising the DNA and a host cell comprising the expression vector comprising the DNA and a host cell comprising the cyperaring a pharmaceutical for preventing and/or treating allergy, or in expression vector comprising relevance, safety or outcome of therapy or a subject, where an IgE containing sample of the subject is mixed with the recombinant allergen and assessed for the level of reactivity between the IgE in the sample and the recombinant allergen or latergen o invention relates to a recombinant allergen (I) which is a mutant of e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic anaphylaxis. The present sequence represents a recombinant allergen of the invention. Note: The present sequence was not shown in the indexer using information in the specification but was created by the indexer using infespecification and the corresponding wild-type sequence

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Gabs

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Sequence 222 AA;

ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120 ELVDCANQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAEEQSCRRPNAQRFGISNYCQIY 120 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180 PPNVNKIREALAQTHSAIAVIIGIKDLEARHYDGQTIIQEDNGYQTNYHAVNIVGYSNA 180 9 9 TNACSINGNAPAEIDLROMETVTPIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ 1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ Gaps ö Query Match 96.3%; Score 1161; DB 5; Length 222; Best Local Similarity 96.4%; Pred. No. 3.2e-122; Matches 214; Conservative 2; Mismatches 6; IndelB (61 121 121

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Spangfort MD;
                                        House dust mite allergen Der p 1 mutant #3.
                                                                                                                                                  Nedergaard Larsen J,
          ABG67026 standard; protein; 222 AA
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                                                                       Dermatophagoides pteronyssinus
                                                                                                         16-NOV-2001; 2001WO-DK000764.
                                                                                                                   16-NOV-2000; 2000DK-0001718.
16-NOV-2000; 2000US-0249361P.
14-JUN-2001; 2001US-0298170P.
                              (first entry)
                                                                                                                                        (ALKA-) ALK-ABELLO AS
                                                                                                                                                            WPI: 2002-508328/54
                                                                                                                                                 Holm J, Ipsen H,
                                                                                                                                                                 N-PSDB; ABK95642
                                                                                      WO200240676-A2
                              24-SEP-2002
                                                                                               23-MAY-2002
                                                                            Synthetic.
                    ABG67026;
RESULT 15
ABG67026
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completed: May 19, 2005, 17:39:01 Best Local Similarity 96.4 Matches 214; Conservative Job time : 163 secs Search ò 셤 셤 ð ò ð The invention relates to a recombinant allergen (I) which is a mutant of a naturally occurring allergen, where the mutant allergen has at least (four primary mutations, which each reduce the specific immunoglobulin E (19E) binding capability of the mutated allergen as compared to the IgE binding capability of the naturally occurring allergen, where each binding capability of the naturally occurring allergen, where each binding capability of the naturally occurring allergen, where each cedidue with another residue, which does not occur in the same position in the amino acid sequence of any known homologous procein within the craxmonnic species from which the naturally occurring allergen originates, at least 15 Angstrom, and the primary mutations are placed in such a manner that at least one circular surface region with a area of 800 angstrom 2 comprises no mutation. Also included are a composition comprising two or more of the recombinant allergens, where the variant allergen in at least one of the other variants, and for each variant not secondary mutation; a DNA sequence encodiary mutation; a DNA sequence encodiary mutation; a DNA sequence encodiary mutation; a box sequence or hybridising the absent primary mutation; a DNA sequence encodiary mutation; a period to it under stringent conditions, where the derivative, partial sequence or degenerated sequence, or a sequence encodes a peptide having at least one B cell epitope; and expension vector comprising the DNA and a host cell comprising the C vector. The recombinant allergen and assessed for the level of reactivity between the ISE in the sample and the recombinant allergen and assessed for the level of reactivity between the ISE in the sample and the recombinant allergen and assessed for the level of ret the sample and the recombinant allergen are useful for a subject or for the sequence or each allergen or compositions are useful for a subject or for the sequence or preparing a subject of reactivity and reactivity of a subject, for vaccinations or treatment New recombinant mutant allergen, useful for preventing and/or treating allergy, comprises multiple mutations and reduced immunoglobulin E binding affinity. Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever; rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant; vaccine; antiallergic; B cell epitope.

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     a subject
treatment, prevention or alleviation of allergic reactions in a subject e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic anaphylaxis. The present sequence represents a recombinant allergen of the invention. Note: The present sequence was not shown in the specification but was created by the indexer using information in the specification and the corresponding wild-type sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               61 ELVDCASOHGCHGDTIPRGIEXIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY
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                                                                                                                                                                                                                              96.2%; Score 1160; DB 5; Length 222; 96.4%; Pred. No. 4.2e-122;
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                                                                                                                                                                               Sequence 222 AA;
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May 19, 2005, 17:36:23 ; Search time 135 Seconds (without alignments) 550.079 Million cell updates/sec
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1 TNACSINGNAPAEIDLRQMR.....YFAANIDLMMIEEYPYVVIL 222
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(cgn2_6)ptodata/2/pubpaa/US07_PUBCOMB.pep:*

(cgn2_6)ptodata/2/pubpaa/US07_NEW_PUB.pep:*

(cgn2_6)ptodata/2/pubpaa/US06_NEW_PUB.pep:*

(cgn2_6)ptodata/2/pubpaa/US06_NEW_PUB.pep:*

(cgn2_6)ptodata/2/pubpaa/US07_NEW_PUB.pep:*

(cgn2_6)ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Score Match Length DB	Length		Ä.	TI.	Description
٠:	To Carden	٠.	3		
100.0			10	US-09-867-159A-2	Sequence 2, Appli
99.5			14	US-10-001-245-88	Sequence 88, Appl
96.4			14	US-10-001-245-26	26,
96.3			14	US-10-001-245-18	Sequence 18, Appl
96.3			14	US-10-001-245-20	20,
96.3			14	US-10-001-245-24	Sequence 24, Appl
96.2			17	US-10-892-543-5	'n
1.96			14	US-10-001-245-22	22,
95.9			14	US-10-001-245-14	14,
95.9			14	US-10-001-245-16	16,
94.8			14	US-10-001-245-30	30,
1142 94.7 222			14	US-10-001-245-28	Sequence 28, Appl
93.9			14	US-10-001-245-34	Sequence 34, Appl

Seguence 32, Appl	95,	184,	185	'n	7 '06	٠.	89,	~	•	٠.		•	N	4	m	ě	Sequence 3, Appli	3, 4	ä	22,	22,		Sequence 151, App	159,					45098	Sequence 155, App	Sequence 57524, A
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US-10-001-245-3	US-09-847-208-9	US-10-001-245-1	US-10-001-245-1	US-10-360-101-2	US-09-972-211-90	US-10-096-625-9	US-09-972-211-8	US-10-096-625-8	US-10-466-110-7	US-10-635-398-9	US-10-273-577-5	US-10-425-114-4	US-10-273-577-2	US-10-273-577-4	US-10-273-577-3	US-09-462-846-3	US-10-773-387-3	US-10-773-914-3	US-10-219-220-15	US-10-872-198-22	US-10-872-197A-2	US-10-425-114-53	US-10-219-220-15	US-10-219-220-15	10-425-114	0-767-701	US-10-767-701-3683	US-10-219-220-17	-701-4	US-10-219-220-15	US-10-425-114-5
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93.9	81.5	81.5	78.3	25.1	24.7	24.7	24.4	24.4	23.4	23.3	23.1	22.7	22.5	22.3	21.7	21.1	21.1	21.1	20.9	20.5	20.5	19.5	17.5	17.2	17.1	17.0	16.9	16.7	16.5	16.4	16.3
1132	982.5	982.5	944.5	303	297.5	297.5	294.5	294.5	282.5	280.5	278.5	274	271.5	268.5	261.5	254	254	254	251.5	247	247	235	211	208	206	205.5	204	201	199.5	197.5	196
14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
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0
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100.0%; Score 1206; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 222; Conservative 0; Mismatches 0;
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SEQ ID NO 18
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61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
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                                                                                                                                                                                                                                                                                                                  Sequence 88, Application US/10001245

Publication No. US20030175312A1

GENERAL INFORMATION:

APPLICANT: HOLM, Jens

APPLICANT: HOLM, Jens

APPLICANT: LARSEN, Henrik

APPLICANT: LARSEN, Jorgen N.

APPLICANT: LARSEN, Jorgen N.

TITLE OF INVENTION: NO. US20030175312A1e1 mutant allergens

FILE REFERENCE: 4305/14942-US2

CURRENT APPLICATION NUMBER: US 40/209,170

PRIOR PILING DATE: 2001-11-15

PRIOR PILING DATE: 2001-06-14

PRIOR PILING DATE: 2001-06-14

PRIOR PILING DATE: 2000-11-16

NUMBER OF SEQ ID NOS: 217

SOFTWARE: PatentIn version 3.1

SEQ ID NO 88

LENGTH: 222
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| Sequence 26, Application No. US20030175312A1
| GENERAL INFORMATION:
| APPLICANT: HOLM, Jens
| APPLICANT: LARSEN Jorgen N. APPLICANT: PARAMETORY, Michael D. TITLE OF INVENTION NO. US20030175312A1e1 mutant allergens FILE REFERENCE: 4305/14942-US2
| CURRENT APPLICATION NUMBER: US/10/001,245
| CURRENT FILING DATE: 2001-11-15
| PRIOR FILING DATE: 2001-06-14
                                                                                                                                                               QGVDYWIVRNSWDTNWGDNGYGYFAANIDLAMMIEEYPYVVIL 222
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US-10-001-245-18

US-10-001-245-18

Sequence 18, Application US/10001245

Publication No. US20030175312A1

GENERAL INFORMATION:

APPLICANT: HOLM, Jens

APPLICANT: LARSEN, Henrik

APPLICANT: LARSEN, Jorgen N.

APPLICANT: SPANGFORT, Michael D.

TILLE OF INVENTION: NO. US20030175312A1e1 mutant allergens

FILE REFERRNCE: 4305/14942-US2

CURRENT FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: US 60/298,170

PRIOR PILING DATE: 2001-06-14

PRIOR FILING DATE: 2000-11-16

NUMBER OF SEQ ID NOS: 217

SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                           Indels
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96.3%; Score 1161; DB 14;
Best Local Similarity 96.4%; Pred. No. 7e-114;
Matches 214; Conservative 3; Mismatches 5;
                                                                                                                                                                                                                                                                   Score 1162; DB 14;
Pred, No. 5.5e-114;
3; Mismatches 5;
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US-10-001-245-26
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     60/249,361
PRIOR APPLICATION NUMBER: US 6(
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 222
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 96.4%;
Matches 214; Conservative
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Query Match
Best Local Similarity 96.4°
Matches 214; Conservative
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APPLICANT: IPSEN, Henrik
        US-10-001-245-24
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APPLICANT: HOLM, Jens
APPLICANT: IPSEN, Henrik
APPLICANT: IPSEN, Henrik
FIGURANT: LARSEN, Josen N.
APPLICANT: LARSEN, Josen N.
APPLICANT: LARSEN, Josen N.
TITLE OF INVENTION: No. US20030175312Alel mutant allergens
FILE REPERENCE: 4305/Ha42-US2
CURRENT APPLICATION NUMBER: US510/001,245
CURRENT FILING DATE: 2001-11-15
FRIOR APPLICATION NUMBER: US 60/298,170
FRIOR PRILING DATE: 2001-06-14
FRIOR PILING DATE: 2001-06-14
FRIOR APPLICATION NUMBER: US 60/249,361
FRIOR APPLICATION NUMBER: US 60/249,361
FRIOR SEQ ID NOS: 217
SOFTWARE: Patent In version 3.1
SSO ID NO 24
LENDTH: 222
                                                                                                                                                                   APPLICANT: HOLM, JOHNS
APPLICANT: HOLM, JOHNS
APPLICANT: LARSEN, Henrik
APPLICANT: LARSEN, Jorgen N.
APPLICANT: LARSEN, Jorgen N.
APPLICANT: SPANGFORT, Michael D.
TITLE OF INVENTION: No. US20030175312A1el mutant allergens
FILE REFERENCE: 4305/11942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/299,170
PRIOR FILING DATE: 2000-10-6-14
PRIOR APPLICATION NUMBER: US 60/299,361
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
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181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
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ORGANISM: Dermatophagoides pteronyssinus
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                                                                                                                   ; Sequence 20, Application US/10001245; Publication No. US20030175312A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 214; Conservative
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Best Local Similarity
                                                                                               US-10-001-245-20
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US-10-001-245-24
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APPLICANT: Best, Elaine A.
APPLICANT: Best, Elaine A.
APPLICANT: Best, Elaine A.
APPLICANT: Best, Elaine A.
TITLE OF INVENTION: VARIANTS OF MITE GROUP 1 ALLERGENS FOR THE TREATMENT OF HOUSE
TITLE OF INVENTION: DUST MITE ALLERGY.
FILE REFERENCE: AL-10
CURRENT PEPLICATION NUMBER: US/10/892,543
CURRENT FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: 60/487,812
PRIOR FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 5
LENGTH: 218
                                                                                                                                                                                                                                    61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
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Length 222;
                                                             Indels
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Score 1161; DB 14;
Pred. No. 7e-114;
2; Mismatches 6;
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   96.3%;
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US-10-001-245-16
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APPLICANT: LARSEN, Jorgen N.
APPLICANT: SPANGFORT, Michael D.
TITLE OF INVENTION: NO. US20030175312A1el mutant allergens
FILE REFERENCE: 4305/1H942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
CURRENT FILING DATE: 2001-11-15
PRIOR PILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/298,170
PRIOR PILING DATE: 2001-06-14
PRIOR PILING DATE: 2001-06-14
PRIOR PILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PATCHTN version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: IPSEN, Jenzik
APPLICANT: IPSEN, Jorgen N.
APPLICANT: LARSEN, Jorgen N.
APPLICANT: LARSEN, Jorgen N.
APPLICANT: LARSEN, Jorgen N.
TITLE OF INVENTION: No. U820030175312A1e1 mutant allergens
FILE REFERENCE: 4305/11942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
CURRENT FILING DATE: 2010-11-15
PRIOR APPLICATION NUMBER: US 60/298,170
PRIOR FILING DATE: 2000-16-14
PRIOR FILING DATE: 2000-11-16
NUMBER: OF SEQ ID NOS: 217
SOOTWARE: PALENTIN VERSION 3.1
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Pred. No. 1.1e-113;
3; Mismatches 5;
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ORGANISM: Dermatophagoides pteronyssinus
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Publication No. US20030175312A1
GENERAL INFORMATION:
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Best Local Similarity 96.4%;
Matches 214; Conservative
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US-10-001-245-14
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LENGTH: 222
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61 ELVDCASQHGCHGDTIPEGIEXIQHNGVVQESYXRVVAQEQSCRRPNAQRFGISNYCQIY 120
                                                                                                                            121 PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGQTIIQEDNGYQTNYHAVNIVGYSNA 180
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                                                                                       121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
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Best Local Similarity 96.4%; Pred. No. 1.8e-113;
Matches 214; Conservative 2; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: INCIPATION Henrik
APPLICANT: LARSEN, Jorgen N.
APPLICANT: LARSEN, Jorgen N.
APPLICANT: SPANGFORT, Michael D.
TITLE OF INVERTION: NO. US20030175312A1el mutant allergens
FILE REFERENCE: 4305/1H942-US2
CURRENT APPLICATION NUMBER: US 6/10/001,245
CURRENT APPLICATION NUMBER: US 6/298,170
PRIOR FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
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Publication No. US20030175312A1
GENERAL INFORMATION:
APPLICANT: HOLM, Jens
APPLICANT: LARSEN, Henrik
APPLICANT: SPANGFORT, Michael D.
TITLE OF INVENTION: No. US20030175312A1el mutant allergens
FILE REFERENCE: 4305/H1942-052
CURRENT APPLICANT NUMBER: US/10/001,245
CURRENT FILING DATE: 2001-11-15
                                                                                                                                                                                                                181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                                                                                                                                  181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
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PRIOR FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/10001245
Publication No. US20030175312A1
GENERAL INFORMATION:
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SEQ ID NO 16
LENGTH: 222
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61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
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GENERAL IN CACALLACAT.

APPLICANT: IPSEN, Henrik

APPLICANT: IPSEN, Henrik

APPLICANT: IPSEN, Henrik

FURLE APPLICANT: APPLICANT: Michael D.

TITLE OF INVENTION: No. US20030175312A1el mutant allergens

FILE REFERENCE: 4305/H942-US2

CURRENT APPLICATION NUMBER: US 60/298,170

FRIOR PELING DATE: 2001-11-15

FRIOR PELING DATE: 2001-06-14

FRIOR FILING DATE: 2001-11-16

FRIOR FILING DATE: 2001-06-14

FRIOR FILING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 217

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 34

LENGTH: 222
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APPLICANT: IDARSEN, Jorgen N.
APPLICANT: IPREN, Jorgen N.
APPLICANT: IPREN, Jorgen N.
TITLE CANT: SPANGFORT, Michael D.
TITLE OF INVENTION: NO. US20030175312Alel mutant allergens
FILE REFERENCE: 4305/1H942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/299,170
PRIOR FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PARCHIN VERSION 3.1
SEQ ID NO 32
LENGTH: 222
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   181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLAMIEEYPYVVIL 222
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ORGANISM: Dermatophagoides pteronyssinus
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US-10-001-245-34
                                                                                                                                                                      Sequence 34, Application US/10001245
Publication No. US20030175312A1
GENERAL INFORMATION:
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US-10-001-245-32
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APPLICANT: HOLM, Jens
APPLICANT: HOLM, Jorgan N.
APPLICANT: LARSEN, Jorgan N.
APPLICANT: LARSEN, Jorgan N.
TITLE OF INVENTION: No. US20030175312Alel mutant allergens
TITLE OF INVENTION: No. US20030175312Alel mutant allergens
FILE REFERENCE: 4305/1H942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
FRIOR APPLICATION NUMBER: US 60/299,170
PRIOR PILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/249,361
PRIOR FILING DATE: 2000-01-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
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ORGANISM: Dermatophagoides pteronyssinus
PRIOR APPLICATION NUMBER: US 60/249,361
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 95.0
Matches 211; Conservative
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US-10-001-245-28
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                                                                                                               SEQ ID NO 30
LENGTH: 222
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US-10-001-245-32

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61 QELVDCASQNGCHGDTIPRGIEYIQQNGVVQEHYYPYVAREQSCHRPNAQRYGLKNYCQI 120
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Query Match 93.9%; Score 1132; DB 14; Length 222; Best Local Similarity 94.6%; Pred. No. 8e-111; Matches 210; Conservative 3; Mismatches 9; Indels 0
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US-09-847-208-95
is Sequence 95, Application US/09847208
is Publication No. US20030082190A1
is Publication No. US20030082190A1
is APPLICANT: Saxon, Andrew
is APPLICANT: Zhang, Ke
is APPLICANT: Zhang, Ke
is APPLICANT: Zhang, Ke
is APPLICANT: APPLICANT: PILIN, Daocheng
is TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
is TITLE OF INVENTION: 19E-MEDIATED ALLERGIC DISEASES
is FILE REFERENCE: UCF. 0.02A
is CURRENT APPLICATION NUMBER: US/09/847,208
is CURRENT FILING DATE: 2001-05-01
is NUMBER OF SEQ ID NOS: 177
is SOFTWARE: FastSEQ for Windows Version 4.0
is SEQ ID NO 95
is LENGTH: 211
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US-09-847-208-95
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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Maximum Match 100%
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119, App
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MEDIUM TYPE: FIDEDPY disk

COMPUTER: D2109

COMPUTER: PEDPOPY DISK

COMPUTER: PEDPOPY DISK

COMPUTER: ASCIT TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/945,288

FILING DATE: 199220910

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 580,655

FILING DATE: 11 SEPTEMBER: 1990

APPLICATION NUMBER: 459,642

PRIOR DATE: 11 SEPTEMBER: 1990

APPLICATION NUMBER: P36,207

REGISTRATION NUMBER: P36,207

REGISTRATION NUMBER: P36,207

REFERENCE/OCKET NUMBER: IPC-010CC (IMI-024)

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FOR SEQ 1D NO: 11:

SEQUENCE: CATABACTERISTICS:

LENGRAM: 2227-5941

SEQUENCE: CHARACTERISTICS:

LENGRAM: 2227-5941
US-08-482-142-193

US-08-478-572-193

US-08-841-296-193

US-08-821-994-78

US-09-325-932A-151

US-09-325-932A-155

US-09-325-932A-145

US-09-325-932A-145

US-09-325-932A-145

US-08-821-994-45

US-08-821-994-45

US-08-478-572-39

US-08-478-572-39

US-08-478-572-39

US-08-478-572-39

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US-08-482-142-39

US-08-482-142-39

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TELECOMMUNICATION INFORMATION
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US-08-461-809-11
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97.7%; Pred. No. 2.5e-126;
iive 0; Mismatches 5; Indels
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/945,288
FILING DATE: 10 SEPTEMBER 1992
APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INPORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1PC-010CC (IMI-024)
LOCATION: 81
OTHER INFORMATION: /label=Xaa is Glu or Lys
FEATURE:
                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: 215
COTHER INFORMATION: /label=Xaa is Glu or Gln
US-07-945-288-11
                                                                                        LOCATION: 124
OTHER INFORMATION: /labelexaa is Ala or Val
                                                                                                                                                         NAME/KEY: misc feature
LOCATION: 136
OTHER INFORMATION: /label=Xaa is Ser
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TITLE OF INVENTION: T CELL EPITOPES OF
TITLE OF INVENTION: DERMATOPHAGOIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,831
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Patent No. 5552142
GENERAL INFORMATION:
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                     NAME/KEY: misc feature
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Matches 217; Conservative
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61 ELVDCASQHGCHGDTIPRGIXYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ
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Patent No. 5770202
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM TITLE OF INVENTION: DERMATOPHAGOIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
97.6%; Score 1177; DB 1;
Best Local Similarity 97.7%; Pred. No. 2.5e-126;
Matches 217; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc feature
; LOCATION: 215
; OTHER INFORMATION: /label=Xaa is Glu or Gln
US-08-462-831-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: 136
OTHER INFORMATION: /label=Xaa is Ser or Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /label=Xaa is Ala or
                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 81
OTHER INFORMATION: /label=Xaa is Glu FEATURE:
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                        LOCATION: 50
OTHER INFORMATION: /label=Xaa is His
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                      LENGTH: 222 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: 50
                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
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COUNTRY: US
ZIP: 02109
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T CELL EPITOPES OF THE MAJOR ALLERGENS FROM DERMATOPHAGOIDES
                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: TAKE
SOFTWARE: ASCII TEXT
CURRENT APPLICATION NUMBER: US/08/461,441
FILING DATE:
CLASSIFICATION NUMBER: US 07/945,288
FILING DATE: 10 SEPTEMBER 1992
APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: 16C-010CC (IMI-024)
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
TENDONE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /label=Xaa is Glu FEATURE:
           TITLE OF INVENTION: T CELL EPITOPES C
TITLE OF INVENTION: DERMATOPHAGOIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 222 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
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LOCATION: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                       ZIP: 02109
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                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ELVDCASQHGCHGDTIPRGIXYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGVDYWIVRNSWDTNWGDNGYGYFAANIDLAMIEXYPYVVIL 222
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,809
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
APPLICATION NUMBER: 13 FEBRUARY 1990
APPLICATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1PC-010CC (IMI-024)
TELECHONE: (617) 227-7400
TELECHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ 1D NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: 136
OTHER INFORMATION: /label=Xaa is Ser or Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) LOCATION: 215
; OTHER INFORMATION: /label=Xaa is Glu or Gln
US-08-461-809-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /label=Xaa is His or Tyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 222 amino acids
TYPE: amino acid
TOPOLOGY: linear
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LOCATION: 124
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61 ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.6%; Score 1177; DB 1; Length 222; Best Local Similarity 97.7%; Pred. No. 2.5e-126; Matches 217; Conservative 0; Mismatches 5; Indels
LOCATION: 50
OTHER INFORMATION: /label=xaa is His or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                i.CCATION: 215
GOTHER INFORMATION: /label=Xaa is Glu or Gln
US-08-461-441-11
                                                                                                                                                                                                                                                                                                        LOCATION: 136
OTHER INFORMATION: /label=Xaa is Ser or Thr
                                                                                                                                                                                                                            OTHER INFORMATION: /label=Xaa is Ala or Val
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RESULT 4
US-08-461-441-11
; Sequence 11, Application US/08461441
; Patent No. 5773002
; GENERAL INFORMATION:

APPLICANT:

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Gaps

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5; Indels

Matches

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ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                          61 ELVDCASQHGCHGDTIPRGIXXIQHNGVVQESYXRYVAREQSCRRPNAQRFGISNYCQIY 120
                                                                                                                                                                                                                     PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                                                                                 1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQ 60
                                                                           1 TNACSINGNAPAEIDLRQMRTVTPIRMQGGGGSCWAFSGVAATESAYLAXRNQSLDLAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mai-chang
APPLICANT: Rogers, Bruce
APPLICANT: Pranzen, Henry
APPLICANT: Pranzen, Henry
APPLICANT: Bvans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: T CELL EPITOPES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
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                                                                                                                                                                                                                                                                                                          181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                                                                                                                                                                                                                   181 QGVDYMIVRNSWDTNWGDNGYGYFAANIDLAMIEXYPYVVIL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION STREET: 610 LINCOLN STREET CITY: WALTHAM STATE: MA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 372.5; DB 2;
Pred. No. 2.2e-34;
8; Mismatches 14;
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,142
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 195, Application US/08482142
Patent No. 5820862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 466-6040 INFORMATION FOR SEQ ID NO: 195:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.6%;
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Garman, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
  217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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121 PPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                           121 PPNXNKIREALAQTHXAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA 180
                                                                                                                                                                                   RESULT 5
PCT-US93-08518-11
| Sequence 11, Application PC/TUS9308518
| GRUERAL INFORMATION:
| APPLICANT:
| TITLE OF INVENTION:
| TITLE OF INVENTION: DERMATOPHAGOIDES
| NUMBER OF SEQUENCES: 13
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: LAHIVE & COCKFIELD
| STREET: & OSTON TE STREET, SUITE 510
| CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 222;
                                                                                                                 181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEXYPYVVIL 222
                                                                                      181 QGVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/945,288
FILING DATE: US SEPTEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISCTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1PC-010CC (IMI-024)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
TELEPHONE: (617) 227-7401
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.6%; Score 1177; DB 5; 97.7%; Pred. No. 2.5e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc feature
LOCATION: 215
LOCATION: 215
PCT-US93-08518-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 50
OTHER INFORMATION: /label=Xaa is His or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 81
OTHER INFORMATION: /label=Xaa is Glu or Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 124
OTHER INFORMATION: /label=Xaa is Ala or Val
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LOCATION: 136
OTHER INFORMATION: /label=Xaa is Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 222 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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CLASSIFICATION:
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Gaps

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68 EQSCRRPNAQQLE----AVFEANQNTKTAKIE--IKASIDGLEVIIGIKDLAFRHYDG 120
    68 EQSCRRPNAQQLE----AVFEANQNTKTAKIE--IKASIDGLEVIIGIKDLDAFRHYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 EQSCRRPNAQRFGISNYCQIYPPNAN----KIREALAQTHSAIAVIIGIKDLDAFRHYDG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 VAATESAYLAYRNTSLDLSEQELVD-------EYIQHNGVVQESYXRYVAR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 VAATESAYLAHRNQSLDLAEQELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
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                                                                                                                                                                                                                                 APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
NUMBER OF SEQUENCES: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLM STREET
CITY: WALTHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 372.5; DB 3
Pred. No. 2.2e-34;
8; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,296
                                                                                                                                                                          Sequence 195, Application US/08484296
Patent No. 6268491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/445,307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: CRAIG, ANNE I. REGISTRATION NUMBER: 32,976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 466-6040 INFORMATION FOR SEQ ID NO: 195:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.9%;
Best Local Similarity 62.6%;
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                         156 RTIIQRDNGYQ 166
                                                             |||||||||||
121 RTIIQRDNGYQ 131
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121 RTIIQRDNGYQ 131
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                                                                                                        68 EQSCRRPNAQQLE-----AVFEANQNTKTAKIE--IKASIDGLEVIIGIKDLDAFRHYDG 120
                                                                           EQSCRRPNAQRFGISNYCQIYPPNAN----KIREALAQTHSAIAVIIGIKDLDAFRHYDG 155
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40 VAATESAYLAHRNQSLDLAEQELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 VAATESAYLAHRNQSLDLAEQELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.9%; Score 372.5; DB 2; Length 181; 62.6%; Pred. No. 2.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMULOGIC PHARMACEUTICAL CORPORATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,572
                        24 VAATESAYLAYRNTSLDLSEQELVD-
                                                                                                                                                                                                                                                                                               Sequence 195, Application US/08478572
Patent No. 5968526
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,307
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (6.17) 466-6000
TELEPAX: (6.17) 466-6040
INFORMATION FOR SEQ ID NO: 195:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32,976
                                                                                                                                                                                                                                                                                                                                                      Garman, Richard
Greenstein, Julia
Kuo, Mei-chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F: 610 LINCOLN STREET WALTHAM
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                      Franzen, Henry
Chen, Xian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    Rogers, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                  RTIIQRDNGYQ 166
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ADDRESSEE: IMMULOGIC
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 82; Conserva
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APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                          RESULT 7
US-08-478-572-195
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Greenstein, Julia
Kuo, Mei-chang
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                                                             Franzen, Henry
                                       Rogers, Bruce
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Best Local Similarity 48.8
Matches 79; Conservative
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; MOLECULE TYPE: protein
US-08-478-572-197
                                                                                Chen, Xian
                                                                                                                                                                                                                                                                        WALTHAM
                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                        CITY: WALS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 SINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAHRNQSLDLAEQELVD
                                                                        GENERAL INFORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Franzen, Henry
APPLICANT: Franzen, Henry
APPLICANT: Franzen, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: PROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 NKIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQ 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --IIGIKDLDAFRHYDGRTIIQRDNGYQ 102
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0;
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Pred. No. 2.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,142
FILING DATE: 07-UN-1995
CLASSIERCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REGISTRATION NUMBER: 017.6US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 466-6000
                                     Sequence 197, Application US/08482142
Patent No. 5820862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.4%;
Best Local Similarity 48.8%;
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 181 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: MA
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US-08-478-572-197
               US-08-482-142-197
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; Sequence 197, Application US/08478572; Patent No. 5968526

GENERAL INFORMATION

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WENTLOANT: NOW WEI-THAN ALLENGENS

APPLICANT: Promach Herry
APPLICANT: Promach Herry
APPLICANT: Chan State
APPLICANT: Chan APPLICANT:
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NOVEL FILARIID NEMATODE CYSTEINE PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 QHGCHGDTIPRGIEYIQHNGVVQESYYRYV--AREQSCRRPNAQRFGISNYCQIYPPNAN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 KIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGY.--SNAQGV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 NNGCHGGFMNPAFYYASKAGIASEAKYPYVHTARRTCYWRKDIVAATDNGYTRIQQGDEK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 PAEIDLROMRIVIPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDCA---S 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 PKYYDWRKRGYVTPAKEQGLCGSCYAFAAAAALEAYNKKTKNKLLDLSPQNILDCTWDLG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 215;
                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 24.5%; Score 295; DB 3; Best Local Similarity 35.8%; Pred. No. 2.2e-25; Matches 73; Conservative 30; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6419923
GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Grieve, Robert B.
APPLICANT: Grieve, Robert B.
APPLICANT: Frank, Glenn R.
TITLE OF INVENTION: NOVEL FILARIID NEMATODE (TITLE OF INVENTION: PROTEASE PROTEINS, NUCLE: NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS.
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 2618-33-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-0223
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 DYWIVRNSWDTNWGDNGYGYFAAN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/768,619
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                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 215 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / MOLECULE TYPE: protein US-09-005-298-38
                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Colorado COUNTRY: U.S.A.
                      U.S.A.
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STATE: Colora
                                                                                                                                                                                                                                     FILING DATE:
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APPLICANT: Wisnewski, Wancy
APPLICANT: Grieve, Robert B.
APPLICANT: Frank, Glenn R.
APPLICANT: Frank, Glenn R.
TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 CASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIYPPNA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SINGNAPABIDIROMRIVIPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83;
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL BPITOPES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
WUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------EYIQHNGVVQESYYRYVAREQSCRRPNAQ--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.4%; Score 354.5; DB 3;
48.8%; Pred. No. 2.6e-32;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I:
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US
TELECHOME: (617) 466-6000
TELEFAX: (617) 466-6000
TELEFAX: (617) 466-6010
INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 antino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38, Application US/09005298 Patent No. 6365392 GENERAL INFORMATION:
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ADDRESSEE: Sheridan Ross P.C.
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Best Local Similarity 48.87
Best Acas 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-296-197
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colorado
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COUNTRY: US
ZIP: 02154
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US-09-005-298-38
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STATE:
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APPLICANT: Tripp, Cynthia A. APPLICANT: Wishewski, Nancy APPLICANT: Grieve, Robert B. APPLICANT: Grieve, Robert B. APPLICANT: Grieve, Robert B. APPLICANT: Frank, Glenn R. TITLE OF INVENTION: NOVEL FILARIID NEWATODE CYSTEINE TITLE OF INVENTION: PROTEBASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF NUMBER OF SEQUENCES: 46 CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C. ADDRESSEE: Sheridan AROS P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 QHGCHGDTIPRGIEYIQHNGVVQESYYRYV--AREQSCRRPNAQRFGISNYCQIYPPNAN 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 KIREALAQTHSAIAVIIGIKDLD-AFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQGV- 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 PAEIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDCA---S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,619
                                                                                                                                                                                                                                                                                                                                                                                                                23.1%; Score 278; DB 3; 34.8%; Pred. No. 1.9e-23; tive 27; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1700 Lincoln Street, Suite 3500
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CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,036
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAMME: COLINGII, GALY J.
REGISTRATION NUMBER: 32,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 DYWIVRNSWDTNWGDNGYGYFAAN 207
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Patent No. 6419923
GENERAL INFORMATION:
    APPLICATION NUMBER: 08/768,619
                                                                                                       REGISTATION NUMBER: 34,020
REFERENCE/DOCKET NUMBER: 261
TELECOMMUNICATION INFORMATION:
TELEFAX: (303) 863-970
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                   NAME: Connell, Gary J. REGISTRATION NUMBER: 32,020
                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.1%
Best Local Similarity 34.8%
Matches 71; Conservative
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MOLECULE TYPE: protein
US-09-005-298-22
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MEDIUM TYPE: Floppy
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COUNTRY: U.S.A.
ZIP: 80203
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                            FILING DATE:
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TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 QHGCHGDTIPRGIEYIQHNGVVQESYYRYV--AREQSCRRPNAQRFGISNYCQIYPPNAN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 KIREALAQTHSAIAVIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGY--SNAQGV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 NNGCHGGFMNPAFYYASKAGIASEAKYPYVHTÄRRTCYWRKDIVAATDNGYTRIQQGDEK 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 24.5%; Score 295; DB 4; Length 215; Best Local Similarity 35.8%; Pred. No. 2.2e-25; Matches 73; Conservative 30; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/09/005,298 FILING PATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; Mismatches
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1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,619
FILING DATE:
CLASSIFFICATION: 435
RIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
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ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/09005298 Patent No. 6365392
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APPLICANT: Wisnewski, Nancy
APPLICANT: Grieve, Robert B.
APPLICANT: Frank, Glenn R.
                                                                                                                                                                                                                                                                                                                                                                                             : 215 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-768-619-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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US-09-005-298-22
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68 QHGCHGDTIPRGIEYIQHNGVVQESYYRYV--AREQSCRRPNAQRFGISNYCQIYPPNAN 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 KIREALAQTHSAIAVIIGIKDLD-AFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQGV- 183
121 KGLANLWQ----LTVVVGISGYQHDFKFYKS-GVYSSDQCRVPN-HAVLVVGYGTSQKTR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PKYVDWRKRGYVTPAKEQGLCGSCYAFCSCSIRSLIYKKTKNKLLDLSPQNILDCTWDLG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                  11 PABIDLROMRTVTPIRMOGGCGSCWAFSGVAATESAYLAHRNOSLDLAEQELVDCA---S 67
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                 92; Indels 14;
                                                                                                                                                                                                                                                                                                                                Query Match 23.1%; Score 278; DB 4; Length 213; Best Local Similarity 34.8%; Pred. No. 1.9e-23; Matches 71; Conservative 27; Mismatches 92; Indels
REFERENCE/DOCKET NUMBER: 2618-33-C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNE: (303) 863-9700
TELEPRAX: (303) 863-0223
TELEFAX: (303) 863-0223
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: anino acid
TYPE: anino acid
TYPE: anino acid
TYPE: anino acid
STRANDEDNESS:
HODOLOGY: linear
US-08-768-619-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYWIVRNSWDTNWGDNGYGYFAAN 207
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Search completed: May 19, 2005, 17:36:14 Job time: 24 secs

|||||::||| ||| ||||| ||||| ||| DYWIIKNSWGTNWARNGYGYMKRN 198

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 19, 2005, 17:50:19 ; Search time 12 Seconds (without alignments) 80.181 Million cell updates/sec Run on:

US-09-867-159A-3 61 1 RMQGGCGSCN 10 Title: Perfect score:

Scoring table: Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1102 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	napin small chain	formylglycinamide	c-rel protein - ch	polygalacturonase	hypothetical prote		٨th	opain	spinal cord peptid	T-cell receptor be	hypothetical prote	sperm-activating p			sperm-activating p			sperm-activating p				sperm-activating p		sperm-activating p					sperm-activating p
SUMMARIES	ID	S70336	A12016	I50633	D61440	S27873	YFPG	A60957	A61289	A23751	PT0727	S06964	A60527	H60787	F60787	A60787	D60787	B60787	D60588	B60588	C60588	I60527	A60588	A60788	D60527	C39572	F60527	C60527	E60527	G60527
	DB	7	7	7	~	~	٦	7	7	ო	~	7	~	~	~	~	~	~	~	~	~	~	~	~	7	7	~	~	7	7
	Length	10	7	0	10	10	σ	σ	10	٣	9	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
	Query Match	4.4	8.3	1.1	1.1	1.1	5.5	9.5	5.5	6.7	7.9	6.7	6.7	7.9	7.9	6.7	•		6.7		•	•		7.9	7.9	6.7		٠	7.9	7.9
æ	Ma Ma	ň	m	m	m	m	ä	č	či	'n	'n	27	27	'n	74	27	27	'n	27	'n	7	'n	27	7	'n	'n	27	'n	'n	'n
	Score	21	20	19	19	19	18	18	18	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17
	Result No.	-	7	e	4	'n	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26		28	53

4 GGCGSC 9 1 GVCDBC

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sperm-activating p	R-phycoerythrin ga	hypothetical rCL3	hemagglutinin - in	hypothetical prote	polygalacturonase	ubiquitin - rat	cadmium-binding pe								
E39572	D60788	E60788	C60788	F60589	C60589	D60589	160588	B60589	F22565	179564	S51912	A35556	B61440	847552	A33882
~	7	7	0	7	7	~	~	7	0	4	7	~	~	7	7
10	10	10	10	10	10	10	10	10	ın	9	10	10	10	4	S
27.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9	26.2	26.2	26.2	26.2	26.2	24.6	24.6
17	17	17	17	17	17	17	17	17	16	16	16	16	16	15	15
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Cibate: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
Cibate: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
Cibate: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
Cipatesion: S70336
Ribeumann, G.M.; Condron, R.; Thomas, I.; Polya, G.M.
Biochim. Biophys. Acta 1295, 23-33, 1996
A;Title: Purification and sequencing of multiple forms of Brassica napus seed napin smal
A;Reference number: S70336; MUID:96283790; PMID:8679670
A;Accession: S70336
A;Atatus: preliminary
A;Molecule type: protein
A;Aesidues: 1.10 cMED.
A;Cross-references: UNIPROT:Q42469; UNIPROT:Q9S9F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               formylglycinamide ribonucleotide amidotransferase (BC 2.....) - chicken (fragment) C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 05-Unn-1987 #sequence_revision 05-Unn-1987 #text_change 13-Mar-1997
C;Accession: Al2016; B12016
R;Ohnoki, S:/ Hong, B.S.; Buchanan, J.M.
Fed. Proc. 35, 1549, 1976
A;Title: Amino acid sequence at glutamine active site for FGAR-amidotransferase.
A;Reference number: A91459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.4%; Score 21; DB 2; Length 10; Best Local Similarity 66.7%; Pred. No. 3.6e+03; Matches 4; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 32.8%; Score 20; DB 2; Length 7; Best Local Similarity 50.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: protein
A,Residues: 1-7 cOHN>
A,Experimental source: liver, peptide
A,Accession: B12016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: protein
A,Reatdues: 1-5 <OH2.
A,Experimental source: liver, peptide
C,Keywords: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 MQGGCG 7
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protein - chicken (fragment)

A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 1-9 < HAN>

31.1%; 50.0%;

Query Match Best Local Similarity 50.v. 13; Conservative 2 MQGGCG 7 3 VSGGAG 8

а

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A,Molecule type: protein.
A,Residues: 'Z',2-4',Z',6-9 <BAC>
C,Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral in a variety of immunoassays.
C,Comment: See PIR:A60957 (sheep) for discussion of another possible N-terminal modifications. C,Superfamily: thymic factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: A60957
R;Ernstroem, U.; Gafvelin, G.; Rudja, J.M.
Biosci. Rep. 10, 403-412, 1990
A;Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship t A;Reference number: A60957; MUID:91064427; PMID:2249004
A;Reference number: A60957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     r form (thymocyte growth peptide) contains a large, non-peptide blocking group with a hig
C;Superfamily: thymic factor
C;Keywords: blocked amino end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Glx) (in FTS) #status experimental
F;1/Modified site: blocked amino end (Glx) (in thymocyte growth peptide) #status experime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in a variety of immunoassays.
C;Comment: This peptide was isolated in two forms. One form contained the pyrrolidone car
r form (thymocyte growth peptide) contains a large, non-peptide blocking group with a hig
                                                                                                                                                                                                                                                                                                                                                                                                                                                               a peptide isolated from pig serun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: UNIPROT:Q7M3CS
C,Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                             ;Species: Sus scrofa domestica (domestic pig);
pate: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004;
Accession: A015-21 A60983;
Pleau, J.M.; Dardenne, M.; Blouquit, Y.; Bach, J.F.
Biol. Chem. 252, 8045-8047,
Title: Structural study of circulating thymic factor: a peptide isolated;
Reference number: A01523; MUID: 78026571; PMID: 914862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thymocyte growth peptide - sheep
N;Contains: FTS (facteur thymique serique)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.Bach, J.F.; Dardenne, M.; Pleau, J.M.; Rosa, J.
Nature 266, 55-57, 1977
A;Title: Biochemical characterisation of a serum thymic factor.
A;Reference number: A60983; MUID:77123829; PMID:300146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 29.5%; Score 18; DB 2; Length 9; Best Local Similarity 60.0%; Pred. No. 2.8e+05; Matches 3; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; DB 1; Length 9;
Pred. No. 2.8e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                  thymic factor - pig
N,Alternate names: FTS (facteur thymique serique)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: UNIPROT: P01255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: protein
Residues: 1-9 <PLE>
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SCN 5
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D61440
polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
C;Species: Aspergillus sp.
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: D61440
R;Stratilova, E.; Markovic, O.; Skrovinova, D.; Rexova-Benkova, L.; Jornvall, H.
J. Protein Chem. 12, 15-22, 1993
A;Title: Pectinase Aspergillus sp. polygalacturonase: multiplicity, divergence, and struA;Reference number: A61440; MUID:93151962; PMID:8427629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CiSpecies: Mus musculus (house mouse)
CiDate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
CiDate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
CiAccession: $27873
A; Description: LRH-1: A nuclear hormone receptor active in the absence of exogenous liga A; Reference number: $27873
A; Accession: $27873
A; Cross-references: UNIPROT: Q61807; EMBL: M81385; NID: g198872; PIDN: AAA39446.1; PID: g1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: UNIPROT:Q92009; EMBL:X56440; NID:g63338; PIDN:CAA39822.1; PID:g58448
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                                                                                                                                                                      C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150633
R;Hannink, M.; Temin, H.M.
Oncogene 5, 1843-1850, 1990
A;Title: Structure and autoregulation of the c-rel promoter.
A;Reference number: 150633; MUID:91133738; PMID:2284104
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-10
A,Cross-references: UNIPROT:Q7M501
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 2; Length 9; Pred. No. 2.8e+05; 1; Mismatches 2; Indels
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RESULT 5 827873 hypothetical protein 2 LRH-1 5'-region - mouse

7 GSC 9

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sperm-activating peptide (Br-Phe-2 SAP-I) - sea urchin (Tripneustes gratilla)
NyAlternate names: SAP-a; speract; TG-1; TG-9
C; Species: Tripneustes gratilla
C; Species: Tripneustes gratilla
C; Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C; Apr-1993 #sequence_revision 19-Apr-1993 #text_change 18-Aug-2000
C; Apr-1993 #sequence_revision 19-Apr-1993 #text_change 18-Aug-2000
C; Apr-1993 #sequence_revision 19-Apr-1993 #text_change 18-Aug-2000
C; Apr-1993 #sequence_revision 19-Aug-1993 #text_change 18-Aug-2000
C; Apr-1993 #sequence_revision 19-Aug-1993 #text_change 18-Aug-1993 #text_change 18-Aug-1993 #text_line
C; Apr-1993 #sequence_revision 19-Aug-1993 #text_line
C; Apr-1993 #text
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A;Mosidues: 1.10 <a href="Yos">YOS</a>, A; Ritai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Sh
Bjochemistry 30, 6203-6209, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associate:
A;Reference number: A39572; WUID:91283461; PMID:2059627
A;Accession: A39572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 1-10 < YO2>
R; Takao, T.; Yoshino, K.; Suzuki, N.; Shimonishi, Y.
B; Takao, T.; Yoshino, Mass Spectrom. 19, 705-712, 1990
A; Title: Analysis of post-translational modifications of proteins by accurate mass measu A; Reference number: A60973; MUID:91167743; PMID:2076468
                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S06964
R;Roelvink, P.W.; Hontelez, J.G.J.; van Kammen, A.; van den Bos, R.C.
A;Accession: 3, 1441-1447, 1989
A;Title: Nucleotide sequence of the regulatory nifA gene of Rhizobium leguminosarum PRE: A;Reference number: S06964; MUD:90136072; PMID:2693897
A;Accession: S06964
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A;Residues: 1-10 <TAX>
C;Superfamily: unassigned animal peptides
F;2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                    hypothetical protein (nifA 5' region) - Rhizobium leguminosarum (fragment)
C;Species: Rhizobium leguminosarum
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
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Matches 3; Conservative
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Best Local Similarity
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A; Residues: 1-10 <ROE>
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1 RGGFG 5
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4 GGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pinal cord peptide SCP-4 - pig
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Cispacies: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
Cispacies: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
Cispacies: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
Cispacies: 17-Jun-2001 #text_change 15-Mar-2004
Cispacies: 17-Jun-2001 #text_change 15-Mar-2004
Airecession: A23751
Airecess
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PT0727
C;Accession: PT0727
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0727
A;Status: translation not shown
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100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
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A; Residues: 1-6 < FEE>
C; Keywords: T-cell recentor
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A;Residues: 1-10 <LOA>
A;Cross-references: UNIPROT:Q7MOW1
C;Superfamily: streptococcal cysteine proteinase
C;Keywords: cysteine proteinase; hydrolase
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Matches 3; Conservative
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C;Species: Hemicentrotus pulcherrimus
C;Species: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
C;Accession: A60787;
R;Suzuki, N.; Kajiura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.; Comp. Biochem. Physiol. B 89, 687-693, 1988
A;Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentra A;Reference number: A60787; MUID:88242184; PMID:3378407
                                                                                                                   R;Suzuki, N.; Kajiura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H. Comp. Biochem. Physiol. B 89, 687-693, 1988
A;Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrd A;Reference number: A60787; MUID:88242184; PMID:3378407
A;Accession: H60787
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Comp. Biochem. Physiol. B 89, 667-693, 1988
A;Title: Some more apperact derivatives associated with eggs of sea urchins, Pseudocentrd
A;Reference number: A60787; MUID:88242184; PMID:3378407
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C;Comment: This oligopeptide from egg jelly is one of several from this species, all of
at shows some, but not absolute, species restriction.
C;Superfamily: unassigned animal peptides
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A,Residues: 1-10 <SUZ>
A)Crossor references: UNIPROT:Q7M4D6
C;Comment: This oligopeptide from egg jelly is one of several from this species, all at shows some, but not absolute, species restriction.
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C,COmment: This oligopeptide from egg jelly is one of several from this species, all
at shows some, but not absolute, species restriction.
sperm-activating peptide (Thr-5 speract) - sea urchin (Anthocidaris crassispina)
C;Species: Anthocidaris crassispina
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 16-Aug-2004
C;Accession: H60787
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C;Species: Anthocidaris crassispina
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 16-Aug-2004
C;Accession: F60787
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 75.0
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 19, 2005, 17:54:20 ; Search time 111 Seconds (without alignments) 46.133 Million cell updates/sec

US-09-867-159A-3 61 1 RMQGGCGSCN 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

2548 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q6x2s9 homo sapien	Q8wp04 ateles belz	012096 caprine art	O12098 caprine art	012100 caprine art	012102 caprine art	012104 caprine art		Q9x3m2 prochloroco	Q92009 gallus gall	Q7m501 aspergillus		Q96qa7 homo sapien	Q61807 mus musculu	Q8uvw2 oreochromis	Q15890 homo sapien	P01255 sus scrofa	Q9h3y3 homo sapien	Q7m3c5 ovis aries	Q99jf4 mus musculu	Q7m0wl streptococc		P84071 allium asca	Q9y4x6 homo sapien	Q71vb8 homo sapien	Q7m3t4 tripneustes	Q7m3t5 tripneustes	Q7m3t6 tripneustes	Q7m3t7 tripneustes	Q7m3t8 tripneustes	Q7m3t9 tripneustes
SUMMAKIES		QI	Q6X2S9	Q8WP04	012096	012098	012100	012102	012104	P82938	Q9X3M2	092009	Q7M501	Q8NEY9	Q96QA7	Q61807	QBUVW2	Q15890	THYF_PIG	<u>0</u> 9н3 <u>ү</u> 3	Q7M3C5	Q99JF4	Q7M0W1	Q64G36	ASCL_ALLAS	Q9Y4X6	Q71VB8	Q7M3T4	Q7M3T5	Q7M3T6	Q7M3T7	Q7M3T8	Q7M3T9
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NON TER 1 1 SEQÜENCE 9 AA, 922 MW; 21E8644EB7340EB8 CRC64;
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BML; AR375652; AAL31489.1; -.
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SEQÜENCE 10 AA; 901 MW; 22DF477DD87EA5B8 CRC64;
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012096,
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U81441; AAB60836.1; -.
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                                             (TrEMBLrel. 04, Created)
(TrEMBLrel. 04, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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(TrEMBLrel. 04, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11660,
                                                                                                                                                                        Caprine arthritis encephalitis virus (CAEV).
Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11660;
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9 A.
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Urbach E., Chisholm S.W.;

"Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";

Limnol. Oceanog. 43:1615-1630(1998).

EMBL; AF070219; AAD23269.1; -.
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01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
Unknown endosperm protein C (Fragment).
Hordeum vulgare (Barley).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
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DOI=10.1002/1522-2683(200011)21:17<3693::AID-ELPS3693>3.0.CO;2-1;
Kristoffersen H.E., Flengsrud R.;
"Separation and characterization of basic barley seed proteins.";
Electrophoresis 21:3693-3700(2000).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 8.5-9.0, ITS MW IS: 11.9 KDA.
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Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.; Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U81443; AAB60840.1; -.
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WCBI_TaxID=1220;
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Last annotation update)
                                                                                  9 AA; 922 MW; 21E8644EB7340EB8 CRC64;
                                                                                                                       Patch 42.6%; Score 26; DB 2; 1 Local Similarity 66.7%; Pred. No. 1.6e+06; les 4; Conservative 0; Mismatches 2;
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SEQUENCE
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P82938;
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5065;
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divergence, and structural patterns linking fungal, bacterial, and
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Score 20; DB 2; Length 10;
Pred. No. 1.4e+04;
0; Mismatches 3; Indels
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MEDLINE=91133738; PubMed=2284104;
Hannink M., Temin H.M.;
"Structure and autoregulation of the c-rel promoter.";
Oncogene 5:1843-1850(1990).
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Polygalacturonase (EC 3.2.1.15) IV (Fragment)
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Last annotation update)
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J. Protein Chem. 12:15-22(1993).
PIR; D61440; D61440.
NON_TER NON_TER PLANDING PROPERTY PROP
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05-JUL-2004 (TrENBLrel. 27, Last sen
C-rel protein (P66-c-rel) (Fragment)
Name-c-rel proteo-oncogene;
Gallus gallus (Chicken).
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32.8%;
ilarity 62.5%;
Conservative
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SEQUENCE FROM N.A. MEDMed=11741603; DOI=10.1016/S0014-5793(01)03183-0; MEDLINE=21617133; Pubmed=11741603; DOI=10.1016/S0014-5793(01)03183-0; MEDLINE=21617133; Pubmed=11741603; DOI=0.-C., Chow W.-Y.; Kung S.-S., Chen Y.-C., Lin W.-H., Chen C.-C., Chow W.-Y.; "Q/R RNA editing of the AMPA receptor subunit 2 (GRIA2) transcript evolves no later than the appearance of cartilaginous fishes."; ERES Lett. 509:277-281(201).

EMBL, AF350050; AALS7192.1; -.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Perciformes, Labroidei,
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
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GO: GO: 0000877; F: DNA binding; IDA.

GO; GO: 0008206; P: bile acid metabolism; IMP.

GO; GO: 00045632; P: cholesterol homeostasis; IMP.

GO; GO: 0045632; P: cholesterol homeostasis; IMP.

TO AA; 1133 MW; 998B68F5B7244EA5 CRC64;
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Last annotation update)
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
AMPA receptor subunit 2 alpha (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-Alpk:APECD-1; TISSUE-Liver;
MEDLINE-22755858; PubMed=12672674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Alpk:APfCD-1; TISSUE=Liver;
     5
                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                   LRH-1 protein.
Name=Nr5a2; Synonyms=LRH-1;
                                                                                                                                                                                                                           PRELIMINARY;
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     3; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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NCBI_TaxID=8127;
                                                     2 MQGGCG
                                                                                 ::|| |
4 IRGGSG
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     Matches
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BA151A2.1 (Cdc42 guanine exchange factor (GEF) 9 (Collybistin, PEM-2, HPEM-2, KTAA0424)) (Fragment).
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Type II hair-specific keratin (Type II hair keratin) (Fragment)
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                                                                            Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bairwa N.K., Bamezai R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY037552; AAK686881; -.
EMBL; AY203953; AAO63472.1; -.
GO; GO:0005882; C:intermediate filament; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Bairwa N.K., Bamezai R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 10 10
10 AA; 1034 MW; 9B53417EAB45B87E CRC64;
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  10
959 MW; 845236C5A1A9D1AE CRC64;
                                                                    31.1%; Score 19; DB 2;
100.0%; Pred. No. 2e+04;
tive 0; Mismatches 0
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Pred. No. 2e+04;
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whitehead S.;
Submitted (SEP-2001) to the
EMBL; AL451106; CAC88408.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 AA; 1122 MW;
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Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                          3, Conservative
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
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10 AA;
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                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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NON TER
SEQUENCE
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GONEY9
LD GONEYA
AC GONEY
DT 01-OC
DT 01-OC
DT 05-JU
DE TYPE
GN HOMME
GN HOMME
OC EUKAR
OC E
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10 0960A
AC 0960A
DT 01-DE
DT 01-DE
DE BA151
ET SUDMI
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Gaps

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GO; GO:0004872; F:receptor activity; IEA.
Receptor.
NON_TER 1 1
NON_TER 10 10
SEQÜENCE 10 AA; 1153 MW; 721A6E5AAEB866C4 CRC64;
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Search completed: May 19, 2005, 18:15:42 Job time : 114 secs

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protein search, using sw model 1 OM protein

Run on:

May 19, 2005, 17:47:19 ; Search time 141 Seconds (without alignments) 27.430 Million cell updates/sec

US-09-867-159A-3 ritle:

1 RMQGGCGSCN 10 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

465227

seq length: 0 seq length: 10 B B Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 16Dec04:*
1: geneseqp1980s:*
2: qeneseqp1980s geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* .. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	Aao20569 Cysteine	Abb98534 Cysteine	_	Adill045 Somatosta	Adill044 Somatosta		Adf69793 M. tuberc	Adill047 Somatosta	Aag86614 Saccharom	Aaw41566 Human cal	Aab97506 Peptide n	Abb08544 Human HCC	Abu55750 Polylinke	Adf69792 M. tuberc	Aab97503 Peptide n	Aar69298 Gp_IIb/II	Add67499 Specific-	Aaw60340 Tumour ho	Aaw50579 GPIIb/III	Aaw93666 Human bre	Ade25476 Tc-99m la	Aay54962 Peptide l	Aay95503 GPIIb/III	Aab21757 Human bre	Aae06335 Human bre
ΙD	AA020569	ABB98534	AAR77350	ADI11045	ADI11044	ABU55751	ADF69793	ADI11047	AAG86614	AAW41566	AAB97506	ABB08544	ABUSS750	ADF69792	AAB97503	AAR69298	ADD67499	AAW60340	AAW50579	AAW93666	ADE25476	AAY54962	AAY95503	AAB21757	AAE06335
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Length	10	10	80	6	6	6	6	10	10	æ	α	9	9	9	8	10	10	10	10	10	10	10	10	10	10
% Query Match	100.0	100.0	60.7	59.0	59.0	59.0	59.0	59.0	52.5	ö	50.8	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2
Score	61	61	37	36	36	36	36	36	32	31	31	30	30	30	30	30	30	30	30	30	30	30	30	30	30
Result No.	-	7	e	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

9 Human 34P 5 Human 34P 3 Human 34P 1 Human 34P 5 Human 34P	Target Rat H1 8-mer Insuli		4 GPIIb/III 9 GFIIb/IIa 8 Peptide 1 5 HER2/NEU 6 Radiophar 1 Radiophar
Abb51909 Abb51815 Abb51593 Abb51491 Abb51409	Ambor 700 Aaw50403 Aay27435 Aao20971 Aae15661	Abp56100 Adh02887 Adh02888 Aaw06390 Ade25470	Ade25444 Adh59029 Aay58625 Aag88625 Ade6416 Adh58651
ABB51909 ABB51815 ABB51593 ABB51491 ABB51705	AAW52097 AAY27435 AAO20971 AAE15661	ABP56100 ADH02887 ADH02888 AAW06390 ADE25470	ADE25444 ADH59029 AAY54928 AAG88625 ADE6416 ADH58651
0 1 1 1 1 0 0 1 1 0 0 1 1 0 0 1 0 1 0 0 1 0 1 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0	2 8 8 8 8	99888	000000 000000
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26 29 29	1 8 8 8 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	23 24 25 25 25 25 25 25 25 25 25 25 25 25 25	4 4 4 4 4 0 11 5 6 4 5 2

# ALIGNMENTS

Antiallergic; antiinflammatory; antiasthmatic; dermatological; allergen; anti-histamine; histamine synthesis inhibitor; allergic hypersensitivity; allergic asthma; allergic rhinitis; cysteine protease protein; enzyme; atopical eczema; epitope. Cysteine protease epitope peptide region, SEQ ID No 3. AAO20569 standard; peptide; 10 AA 02-JAN-2003 (first entry) AA020569; RESULT 1 AAO20569 

Dermatophagoides pteronyssinus.

WO200278736-A2.

10-OCT-2002.

28-MAR-2002; 2002WO-FR001098.

30-MAR-2001; 2001FR-00004370. 03-MAY-2001; 2001FR-00005929. 29-MAY-2001; 2001US-00867159.

(ANTI-) ANTIALIS SARL.

Trehin Y; Terrasse G, Loria E,

WPI; 2002-750636/81.

Antiallergic compositions containing an anti-histamine, a histamine synthesis inhibitor, and optionally an allergen or nucleic acid coding for the allergen.

Claim 14; Page 11; 32pp; French.

The invention relates to antiallergic compositions containing an anti-histamine, a histamine synthesis inhibitor, and optionally an allergen or isolated nucleic acid molecule that has at least one polynucleotide sequence coding for the allergen, together with a pharmaceutical carrier. The pharmaceutical composition of the invention is useful as a non-specific antiallergic treatment, and also useful in the treatment of allergic hypersensitivity, allergic asthma, allergic rhintis, and allergic and acopical eczema. This sequence represents a peptide of a cysteine protease epitope region relating to the antiallergic

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The sequences given in AAR77350-53 are peptides derived from the canonical Haemonchus contortus cysteine proteinase molecule which were used in the design of the primers given in AAQ94240-43. These primers were used in the cloning of cDNA fragments from the cysteine proteinase gene, such as DM.1, DM.2, DM.3, DM.4, DM.4a and DM.5 (see also AAQ94246-51). The amplified fragments may be expressed in a recombinant cell for the production of antigens. These antigens may be used in the preparation of a vaccine against helminth parasites in a human or non-human animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protective helminth parasite antigen - used in vaccine directed against parasitic nematodes of mammalian gastro-intestinal tract e.g. Haemonchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dihydropyridine/pyridinium salt type redox moiety; retina; lipophilic; antidiabetic; ophthalmological; diabetic retinopathy; growth factor inhibitory activity; somatostanin; somatostatin analogue; octreotide; lanreotide; sequențial metabolism;
                                                                                                                                                         Primer, amplify; polymerase chain reaction; PCR; Haemonchus contortus; cysteine proteinase; DM.2; DM.3; DM.4; human; DM.4a; DM.5; antigen; vaccine; helminth; parasite; DM.1; ruminant; gastro-intestinal tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 2; Length 8;
Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murray J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith WD, Redmond D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Somatostatin analogue peptide SEQ ID NO:60.
                                                                                                                      Cysteine proteinase derived peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MLCW ) MALLINCKRODT VETERINARY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insulin dependent diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 16; Fig 15; 79pp; English.
  AAR77350 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADI11045 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                  94GB-00005925.
94GB-00005990.
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85.7%;
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                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                         Haemonchus contortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-351322/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 OGCCGSC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ94240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8 AA;
                                                                                                                                                                                                                                                                                WO9526402-A1.
                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                           24-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-APR-2004
                                                                             14-MAY-1996
                                                                                                                                                                                                                                                                                                                       05-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Knox DP,
                                      AAR77350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to an antiallergic pharmaceutical composition (I) comprising a pharmaceutical carrier containing an active agent combination of at least two of: an allergen; an antihistramine; and a histramine synthesis inhibitor. (I) is used for treating or preventing allergic hypersensitivity reactions, especially allergic asthma, allergic rhinitis or allergic eczema, in babies, children or adults. The present sequence is a peptide fragment (epitope) of cysteine protease from Dermatophagoides pteronyssinus, which was used as an allergen in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antiallergic composition, useful for preventing and treating e.g. asthma, rhinitis or eczema, containing at least two of allergen, antihistamine and histamine synthesis inhibitor.
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antiallergic; antiasthmatic; antiinflammatory; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunotherapy; allergen; allergic hypersensitivity reaction;
allergic asthma; allergic rhinitis; allergic atopic eczema;
                                                                           100.0%; Score 61; DB 5; Length 10; 100.0%; Pred. No. 0.027; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 61; DB 5; Length 10; 100.0%; Pred. No. 0.027; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trehin Y;
                                                                                                                                                                                                                                                                                              ABB98534 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dermatophagoides pteronyssinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 6; 33pp; French.
compositions of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                   Cysteine protease epitope #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAY-2001; 2001FR-00005929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001FR-00004370
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                              Best Local Similarity 100
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
                                                                                                                                                       RMQGGCGSCN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RMQGGCGSCN 10
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                                                                                                                                                                                              RMOGGCGSCN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Terrasse G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ANTI-) ANTIALIS SARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-735037/80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cysteine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 AA;
                                      Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FR2822709-A1
                                                                                                                                                                                                                                                                                                                                                                            13-DEC-2002
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                                                                                                                                                                                                                                                                                                                                       ABB98534;
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Gaps

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RESULT 3

18-MAR-1999

Bodor NS,

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The present invention describes peptide derivatives (I) comprising a dihydropyridine/pyridinium salt type redox moiety for targeting peptides to the retina, a bulky lipophilic function and an amino cold/dipeptide/tripeptide spacer. Also described: (I) the preparation of (I); and (2) intermediate quaternary salts (II). (I) have antidiabetic and ophthalmological activities. (I) can be used in the treatment or prevention of diabetic retinopathy by delivery of peptides with growth factor inhibitory activity (e.g. somatostatin analogues such as octreotide and lanreotide) to the retina by sequential metabolism. It is envisaged that (I) will be useful in the treatment of insulin dependent diabetes mellitus parients for critical periods in diabetic retinopathy disease progression before laser photocoagulation is indicated, preferably for 1-4 month intervals when a patient is experiencing severe con-proliferative diabetic retinopathy or is found to have low risk diabetic retinopathy. The present sequence represents a somatostatin analogue peptide, which is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polylinker peptide #3 relating to invention of M. tuberculosis antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide derivatives with redox targetor moiety are useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis antigenic polypeptide; immune response; tuberculosis infection; polylinker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 2; Length 9; Pred. No. 1.8e+06; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; SEQ ID NO 59; 186pp; English.
                  Location/Qualifiers
                                                              'note= "Xaa = Trig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of diabetic retinopathy
                                                                                                                                  = OH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU55751 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                              97US-0058423P.
                                                                                                                                                                                                                                                                  98WO-US017987
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83.3%;
                                                                                                                                  /note= "Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAR-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                        (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                  Bodor NS, Grant MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-263364/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                 Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9 AA;
                       Key
Modified-site
                                                                                                                                                                                                                                                                  01-SEP-1998;
                                                                                                                                                                         WO9912572-A1
                                                                                                                                                                                                                                                                                                              10-SEP-1997;
                                                                                                                                                                                                                      18-MAR-1999
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%XCCCCCCCCCCCCCCCX8X44X6X6X6X6X6X6X6X6X6X44444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes peptide derivatives (I) comprising a dihydropyridine/pyridinium salt type redox moiety for targeting peptides to the retina, a bulky lipophilic function and an amino cot dihydroppride/tripeptide spacer. Also described: (I) the preparation of (I); and (2) intermediate quaternary salts (II). (I) have antidiabetic and ophthalmological activities. (I) can be used in the treatment or prevention of diabetic retinopathy by delivery of peptides with growth factor inhibitory activity (e.g. somatostatin analogues such as octreotide and lanreotide) to the retina by sequential metabolism. It is envisaged that (I) will be useful in the treatment of insulin dependent diabetes mellitus patients for critical periods in diabetic retinopathy disease progression before laser photocoagulation is indicated, preferably for 1-4 month intervals when a patient is experiencing severe con-proliferative diabetic retinopathy or is found to have low risk diabetic retinopathy. The present sequence represents a somatostatin analogue peptide, which is used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dihydropyridine/pyridinium salt type redox moiety; retina; lipophilic; antidiabetic; ophthalmological; diabetic retinopathy; growth factor inhibitory activity; somatostatin; somatostatin analogue; octreotide; lanreotide; sequential metabolism; insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide derivatives with redox targetor moiety are useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 2; Length 9; Pred. No. 1.8e+06; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Somatostatin analogue peptide SEQ ID NO:59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; SEQ ID NO 60; 186pp; English.
                Location/Qualifiers
                                                            'note= "Xaa = Nic'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of diabetic retinopathy.
                                                                                                                                /note= "Xaa = OH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADI11044 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                            97US-0058423P
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83.3%;
                                                                                                                                                                                                                                                                98WO-US017987
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Best Local Similarity 83.3.
S. Conservative
                                                                                                                                                                                                                                                                                                                                                      (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-263364/22.
                                                                                                                                                                                                                                                                                                                                                                                                    Grant MB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCGGC 7
                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9 AA;
                                         Modified-site
                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                            10-SEP-1997;
                                                                                                                                                                         WO9912572-A1
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The present invention relates to fusion proteins of Mycobacterium tuberculosis antigens, and the polynucleotide sequences encoding them. The sequences of the invention are useful in a method for preventing tuberculosis by administering to a subject an amount of the fusion protein or the polynucleotide that encodes the fusion protein. Also disclosed is a pharmaceutical composition comprising the fusion protein or the polynucleotide sequence encoding it. The fusion protein induces an immune response to M. tuberculosis and can be used in the diagnosis, prevention, and treatment of tuberculosis infection. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dihydropyridine/pyridinium salt type redox moiety; retina; lipophilic; antidiabetic; ophthalmological; diabetic retinopathy; growth factor inhibitory activity; somatostatin; somatostatin analogue; octreotide; lanreotide; sequential metabolism; insulin dependent diabetes mellitus.
                                                                          New fusion proteins of Mycobacterium tuberculosis for diagnosing, preventing or treating tuberculosis infection or in enhancing immune
                                                                                                                                                                                                                                                                                                                                                                                                                                    59.0%; Score 36; DB 7; Length 9; 83.3%; Pred. No. 1.8e+06; ive 0; Mismatches 1; Indels
Dillon DC, Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Somatostatin analogue peptide SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                          represents a flexible polylinker peptide
                                                                                                                                                    Disclosure; SEQ ID NO 43; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI11047 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Xaa = OH"
                                                                                                               responses in M. tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US017987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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   Skeiky YA,
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                                     WPI; 2003-897524/82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCGGC
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Modified-site
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bodor NS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI11047;
   Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADI11047
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                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of polynucleotide sequences encoding Mycobacterium tuberculosis antigenic polypeptides. The polynucleotide sequences of the invention are useful for treating, preventing, and diagnosing M. tuberculosis infection, for producing M. tuberculosis infection, for producing M. tuberculosis infection, for producing M. tuberculosis secretory polypeptides, for producing DNA vaccines, for presence of bacteria in a biological sample, for inducing and/or presence of bacteria in a biological sample, for inducing and/or ABUS5749 tepresent flexible polylinker peptides. Note: The present sequence is given in the Sequence listing but is not mentioned elsewhere in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M. tuberculosis fusion protein associated flexible polylinker peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                                           Novel isolated mycobacterial polynucleotide, useful for treating, preventing or diagnosing Mycobacterium tuberculosis infection, for producing Mycobacterium tuberculosis secretory polypeptides and DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion protein; Mycobacterium tuberculosis antigen;
tuberculosis infection; immune response; tuberculostatic;
flexible polylinker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.0%; Score 36; DB 6; Length 9; 83.3%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                       Disclosure; Col 89; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADF69793 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-00818112.
97US-00942578.
98US-00025197.
98US-00056556.
98US-00223040.
                                       99US-00470191
                                                                            98US-0113952P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                 (CORI-) CORIXA CORP
                                                                                                                                                                                        WPI; 2003-147072/14.
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                                       23-DEC-1999;
                                                                          24-DEC-1998;
 15-OCT-2002
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30-DEC-1998
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                                                                                                                                                    Skeiky Y;
                                                                                                                                                                                                                                                                                    vaccines
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AAW41566;
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Matches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and
                                                          The present invention describes peptide derivatives (I) comprising a dihydropyridine/pyridinium salt type redox moiety for targeting peptides to the retina, a bulky lipophilic function and an amino acid/dipeptide/tripeptide spacer. Also described: (I) the preparation of (I), and (2) intermediate quaternary salts (II). (I) have antidiabetic and ophthalmological activities. (I) can be used in the treatment or prevention of diabetic retinopathy by delivery of peptides with growth factor inhibitory activity (e.g. somatostatin analogues such as corrected and lanreotide) to the retina by sequential metabolism. It is envisaged that (I) will be useful in the treatment of insulin dependent diabetes mellitus patients for critical periods in diabetic retinopathy
                                                                                                                                                                                                         disease progression before laser photocoagulation is indicated, preferably for 1-4 month intervals when a patient is experiencing severe non-proliferative diabetic retinopathy or is found to have low risk diabetic retinopathy. The present sequence represents a somatostatin analogue peptide, which is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying complementary peptides by analysis of protein and nucleotide sequence databases, useful in drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae; complementary peptide; peptide identification;
                                                                                                                                                                                                                                                                                                                                                           Gaps
 derivatives with redox targetor moiety are useful in the
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                                                                                                                                                                                                                                                                                                                             Score 36; DB 2; Length 10;
Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae peptide, SEQ ID NO: 1563.
                                      Example 10; SEQ ID NO 62; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 245; 488pp; English.
New peptide derivatives with redox
treatment of diabetic retinopathy.
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                                                                                                                                                                                                                                                                                                                                59.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug discovery; drug design.
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3v.,
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roberts GW, Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PROT-) PROTEOM LTD.
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                                                                                                                                                                                                                                                                                                      Sequence 10 AA;
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                                                                                                                                                                                                                                                                               invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human calpain protein and related DNA - useful for drug screening and
                                                                                                                                                                                                                  Gaps
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drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calpain; human; leukocyte; calcium dependent cysteine protease; screening; activator; inhibitor; treatment; prevention; cancer; cerebral apoplexy; cerebral infarction; subarachhoid haemorrhage; Alzheimer's disease; myodystrophy; cataracts; collagen disease; ischaemic heart disease; atherosclerosis; arthritis.
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                                                                                                                                                            Length 10;
                                                                                                                                                                                                             1; Indels
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                                                                                                                                                          Score 32; DB 4; I
Pred. No. 4.3e+02;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW41566 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human calpain partial peptide.
                                                                                                                                                          Similarity 71.4%; 5; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating cancer, stroke, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                 4 VSGGCGS 10
                                                                                                                                                                                                                                                                2 MQGGCGS 8
                                                                                                                                                                                  Local Similarity
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                                                                                                            Sequence 10 AA;
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The present invention discloses new human HCCAl protein, the polymucleotides encoding the polypeptide and the recombinant process to produce the polypeptide. The present invention also discloses the method of applying the medicine composite of the polypeptide in treating liver cancer and other diseases. The present invention also discloses the preparation process of HCCAl protein specific antibody and its application in disgnosing and treating diseases. The present invention also discloses the application of the polynucleotides encoding the new HCCAl protein. The present sequence represents a peptide sequence relating to human HCCAl protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polylinker peptide #2 relating to invention of M. tuberculosis antigens.
                                                                                                                                                                                                                                                                                                                                                                                       New liver cancer up expressing gene for treating liver cancer and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis antigenic polypeptide; immune response; tuberculosis infection; polylinker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.2%; Score 30; DB 5; Length 6; 80.0%; Pred. No. 1.8e+06; cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                           (SHAN-) SHANGHAI DONGFANG LIVER & GALLBLADDER SU.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 5; Page 16 (disclosure); 31pp; Chinese.
                                                   HCCA1; liver cancer; cytostatic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABUS5750 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                        08-MAY-2000; 2000CN+00115595
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               Human HCCAl PCR primer P4
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                                                                                                                                                                                                                                                                                                                  Zeng J,
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                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6465633-B1
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                                                                                                                                                               21-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                          diseases,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of peptide nucleic acids (PNAs) capable of binding to a cell surface receptor, where the oligomer and the peptide are linked by a chemical bond or an amino acid linker. The oligomer may have a polyamide, polythicamide, polysulfinamide or polysulfonamide backbone. The PNAs of the invention can be used in therapy, including the treatment of infections, cancer, autoimmune diseases, renal failure, endocrinological disorders, acromegaly, neurological diseases and sickle cell anaemia. The present sequence is an example of a peptide for use in a PNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel conjugate, useful for killing pathogenic organisms and for inhibiting gene expression, comprising a peptide nucleic acid oligomer conjugated to ligand capable of binding to a cell surface receptor via chemical bond or linker.
                                                                                                                                                             Peptide nucleic acid; PNA; therapy; infection; cancer; restenosis; asthma; autoimmune disorder; endocrinological disorder; renal failure; neurological disease; acromegaly; sickle cell anaemia;
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                                                                                                                                                                                                                                                                                                                                                    /note= "optionally bound to AAH23598"
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "optionally D-form residue"
                                                                                                                           Peptide nucleic acid peptide fragment #4
                                                                                                                                                                                                                                                                                            Location/Qualifiers
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               AAB97506 standard; peptide; 8 AA
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                                                                                                                                                                                                                                                                                                                               /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                     label= OTHER
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                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Basu S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-342005/36.
                                                                                                                                                                                                                     polyamide backbone
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                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8 AA;
                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wickstrom E,
                                                                                        14-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               US6180767-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAY-2002
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                                                                                                                                                                                                                                                        Synthetic,
                                                  AAB97506;
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ABB08544
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Matches

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Gaps

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Basu S;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     GCGSC 9
                                                                                                                                                                                                                                                                                                                                                                                                            1 60660
                                                                                                                                                                                                                                                     Sequence 6 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wickstrom E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-2001
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                                                                                                                                                                                                                                                                                                                                 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB97503;
                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB97503
  & × C C C C C C C C X & S
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                                                                                                                                                                                                       The present invention relates to the isolation of polymucleotide sequences encoding Mycobacterium tuberculosis antigenic polypeptides. The polymucleotide sequences of the invention are useful for treating, preventing, and diagnosing M tuberculosis infection, for producing M tuberculosis secretory polypeptides, for producing DNA vaccines, for diagnostic purposes, as molecular probes or primers to detect the presence of bacteria in a biological sample, for inducing and/or enhancing immune responses to M. tuberculosis, and in gene therapy. BMIS5749-ABUS5754 represent flexible polylinker peptides. Note: The present sequence is given in the Sequence listing but is not mentioned elsewhere in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M. tuberculosis fusion protein associated flexible polylinker peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New fusion proteins of Mycobacterium tuberculosis for diagnosing, preventing or treating tuberculosis infection or in enhancing immune responses in M. tuberculosis.
                                                                        Novel isolated mycobacterial polynucleotide, useful for treating, preventing or diagnosing Mycobacterium tuberculosis infection, for producing Mycobacterium tuberculosis secretory polypeptides and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 6; Length 6;
Pred. No. 1.8e+06;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusion protein, Mycobacterium tuberculosis antigen,
tuberculosis infection, immune response, tuberculostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alderson M,
                                                                                                                                                                        Disclosure; Col 89; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADF69792 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00818112.
97US-00942578.
98US-00025197.
98US-00056556.
98US-00223040.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 80.0
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                                  WPI; 2003-147072/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  flexible polylinker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-897524/82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6 AA;
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18-FEB-1998;
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30-DEC-1998
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Best Local S
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                                                                                                                                      vaccines
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ADF69792

ADF69792

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                                                  The present invention relates to fusion proteins of Mycobacterium tuberculosis antigens, and the polynuclectide sequences encoding them. The sequences of the invention are useful in a method for preventing tuberculosis by administering to a subject an amount of the fusion protein or the polynuclectide that encodes the fusion protein. Also disclosed is a pharmaceutical composition comprising the fusion protein for the polynuclectide sequence encoding it. The fusion protein induces an immune response to M. tuberculosis and can be used in the diagnosis, prevention, and treatment of tuberculosis infection. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= OTHER
/note= "optionally 4-methoxybenzyl-Cys, optionally D-form
residue"
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/note= "optionally modified by benzyl, optionally D-form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "optionally modified by phenylmethoxycarbonyl and resin, optionally D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide nucleic acid; PNA; therapy; infection; cancer; restenosis; asthma; autoimmune disorder; endocrinological disorder; renal failure; neurological disease; acromegaly; sickle cell anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "optionally modified by phenylmethoxycarbonyl optionally D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 7; Lengtn v;
Pred. No. 1.88+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "optionally bound to AAH23598"
Disclosure; SEQ ID NO 42; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                       represents a flexible polylinker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide nucleic acid peptide fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB97503 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.2%;
80.0%;
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SQ Sequence 8 AA;

Query Match

Best Local Similarity 66.7%; Pred. No. 1.8e+06;

Matches 4; Conservative 0; Mismatches 2; Indels

Qy 4 GGGSC 9

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Db 3 GGCSKC 8

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0; Gaps

Search completed: May 19, 2005, 17:59:05 Job time : 147 secs

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Sequence 3, Appli
Sequence 69, Appl
Sequence 60, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 62, Appli
Sequence 62, Appli
Sequence 62, Appli
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Sequence 62, Appl
Sequence 62, Appl
Sequence 42, Appl
Sequence 42, Appl
Sequence 6, Appli
                                                                                                                                                        May 19, 2005, 17:59:41; Search time 89.5 Seconds (without alignments) 37.375 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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5: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-175-833-59
US-10-175-833-60
US-10-175-833-62
US-09-287-849-43
US-10-359-460-43
US-10-359-460-43
US-10-359-460-43
US-10-163-415-2
US-10-163-415-2
US-10-702-228A-62
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US-10-359-460-42
US-10-359-459-6
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Maximum DB seq length: 10
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Sequence 57, Appl Sequence 222, App Sequence 324, App		, 25°,	Seguence 57, Appl Seguence 57, Appl		Sequence 593, App Sequence 4. Appli				2467,	Sequence 3195, Ap	855,	2495,	3217,	4122	822	Sequence 2495, Ap	Seguence 3217, Ap	Sequence 4122, Ap	Sequence 52, Appl		Seguence 2759, Ap	2761	378(	52,	a)
US-09-765-086-57 US-09-779-308-22 US-09-779-308-32		4 US-10-264-374-5	.4 US-10-375-992-57 .5 US-10-264-374-57	US-10-375-992-5		US-10	US-10-149-138-3	US-10-311-129-2	US-10-149-138-2	US-10-149-138-3	US-10-149-138-8	US-10-149-138-2	US-10-149-138-3	US-10-149-138-4	US-10-149-138-8	US-10-149-138-2	6 US-10-149-138-3	9		0 US-09-572	.0 US-09-572-404B-2759			.4 US-10-264-374-52	.4 US-10-375-992-52
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14 15	17	50	21 22	23	4, C.	26	27	28	. 62	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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TITLE OF INVENTION: Anti-allergic pharmaceutical composition containing at least one TITLE OF INVENTION: Anti-allergic pharmaceutical composition containing at least one TITLE OF INVENTION: and at least one anti-histamine compound FILE REPERENCE: B112812018-antialis
CURRENT APPLICATION NUMBER: US/09/867,159A
CURRENT FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: PEPTIDE

CCATTON: (1)..(10)

OTHER INFORMATION: Comprises epitope from cystine protease.
US-09-867-159A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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100.0%; Pred. No. 0.03;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Dermatophagoides pteronyssinus
              Sequence 3, Application US/09867159A Publication No. US20030104013A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 10; Conservative
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JS-09-867-159A-3
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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4 GGCGSC 9
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ORGANISM: Unknown
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NAME/KEY: BINDING
LOCATION: (1)
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                                                                 # APPLICANT: BODOR, Nicholas Stephen
# APPLICANT: BODOR, Nicholas Stephen
# APPLICANT: BARTOLOMEO, Maria
# TITLE OF INVENTION: COMPOUNDS AND METHOD FOR THE PREVENTION AND TREATMENT
# TITLE OF INVENTION: OF DIABETIC RETINOPATHY
# FILE REFERENCE: 028724-109
# CURRENT APPLICATION NUMBER: US/10/175,833
# CURRENT APPLICATION NUMBER: US/09/144,991
# PRIOR FILING DATE: 1998-09-01
# PRIOR FILING DATE: 1997-09-10
# NUMBER OF SEQ ID NOS: 65
# SOFTWARE: Patentin Ver. 2.0
# SEQ ID NO 59
# LENGTH: 7
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US-10-175-833-60

is Sequence 60, Application US/10175833

sequence 60, Application US/10175833

publication No. US20030211981A1

is GENERAL INFORMATION:

is APPLICANT: BODOR, Nicholas Stephen

APPLICANT: BARTOLOMEO, Maria

it TITLE OF INVENTION: COMPOUNDS AND METHOD FOR THE PREVENTION AND TREATMENT

ITLE OF INVENTION: OF DIABETIC RETINOPATHY

TITLE OF INVENTION: OF DIABETIC RETINOPATHY

CURRENT APPLICATION NUMBER: US/10/175,833

CURRENT APPLICATION NUMBER: US/09/144,991

PRIOR APPLICATION NUMBER: US 60/058,423

PRIOR FILING DATE: 1998-09-01

PRIOR FILING DATE: 1997-09-10

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 60
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, OTHER INFORMATION: Description of Unknown Organism:peptide derivative
US-10-175-833-59
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LOCATION: (7)
OTHER INFORMATION: Amino acid 7 is attached by a hydroxide bond.
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COCATION: (3)..(6)
OTHER INFORMATION: attached by a non-peptidal disulfide bond.
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MAME/KEY: BINDING
LOCATION: (1)
OTHER INFORMATION: Amino acid 1 is attached by Nic.
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                Sequence 59, Application US/10175833; Publication No. US20030211981A1; GENERAL INFORMATION:
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Similarity 83.3%;
5; Conservative
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Best Local Similarity
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ORGANISM: Unknown
JS-10-175-833-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
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Sequence 62, Application US/10175833

Publication No. US20030211981A1

GENERAL INFORMATION:

APPLICANT: BODOR, Nicholas Stephen

APPLICANT: BARTOLOMEO, Maria

TITLE OF INVENTION: COMPOUNDS AND METHOD FOR THE PREVENTION AND TREATMENT

TITLE OF INVENTION: OF DIABETIC RETINOPATHY

TITLE OF INVENTION: 028724-109

CURRENT APPLICATION NUMBER: US/10/175,833

CURRENT PILING DATE: 1998-09-0.1

PRIOR FILING DATE: 1998-09-0.1

PRIOR FILING DATE: 1997-09-10

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 62
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; OTHER INFORMATION: Description of Unknown Organism:peptide derivative
US-10-175-833-60
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FEATURE:
NAME/KEY: ENDING
LOCATION: (7)
OTHER INFORMATION: Amino acid 7 is attached by a hydroxide bond.
NAME/KEY: DISULFID
LOCATION: (3)...(6)
OTHER INFORMATION: Cysteine residues at positions 3 and 6 are
OTHER INFORMATION: attached by a non-peptidal disulfide bond.
NAME/KEY: BINDING
LOCATION: (7)
OCHER INFORMATION: Amino acid 7 is attached by a hydroxide bond.
NAME/KEY: DISCLEIDE
LOCATION: (3)...(6)
OTHER INFORMATION: Cysteine residues at positions 3 and 6 are
OTHER INFORMATION: attached by a non-peptidal disulfide bond.
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Pred. No. 1.3e+06;
                                                                                                                                                                                                                                                                       Score 36; DB 15;
Pred. No. 1.3e+06;
0; Mismatches 1
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; Sequence 43, Application US/09287849
; Patent No. US2002009459A1
; GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 93.3
Matches 5, Conservative
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3 GGCGGC 8
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US-1U-259-480-43

US-QUENCE 43, Application US/10359460

Publication No. US20030147911A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Sheiky, Yasir A.W.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: This or Their Uses
FILE REFRENCE: 014058-009020US

CURRENT PAPLICATION NUMBER: US/10/359,460

CURRENT PAPLICATION NUMBER: US/09/287,849

PRIOR FILING DATE: 1999-04-07

PRIOR FILING DATE: 1999-04-07

PRIOR FILING DATE: 1999-04-07

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-04-07

SOFTWARE: PALEATION NUMBER: US 09/223,040

PRIOR FILING DATE: 1998-04-07

PRIOR PRI
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Contact Corporation
TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REPRENCE: 014058-009020US
FILE REPRENCE: 014058-009020US
FURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,23,040
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
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US-09-287-849-43
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.5
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LENGTH: 9
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Sequence 7, Application US/10359459

$ Sequence 7, Application US/10359459

$ Publication No. US20040013677A1

$ CENERAL INFORMATION:

$ APPLICANT: Skelsky, Yasir

$ APPLICANT: Campos-Neco, Antonio

$ TITLE OF INVENTION: and Their Uses

$ TITLE OF INVENTION OF THE USES

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:flexible
; OTHER INFORMATION: polylinker
US-10-359-460-43
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                                                                                                                                                                                                                                                                                                                              Length 9;
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APPLICANT: KNOX, DAVID PATRICK
APPLICANT: SMITH, WILLIAM DAVID
APPLICANT: REDMOND, DIANE
APPLICANT: MURRAY, JACQUELINE
TITLE OF INVENTION: VACCINES AGAINST HELMINTHIC PARASITES
FILE REFERENCE: 1181-264
                                                                                                                                                                                                                                                                                                                          59.0%; Score 36; DB 14;
83.3%; Pred. No. 1.3e+06;
tive 0; Mismatches 1;
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Pred. No. 1.3e+06;
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CURRENT APPLICATION NUMBER: US/10/163,415
CURRENT FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 08/716418
PRIOR FILING DATE: 1996-09-20
PRIOR APPLICATION NUMBER: PCT/GB95/00665
PRIOR APPLICATION NUMBER: GB 9405925.0
PRIOR PILING DATE: 1994-03-25
PRIOR PILING DATE: 1994-03-25
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Publication No. US20030129204A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                             Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                   2 GGCG-CN 7
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                                                                                                                                                                                                                                                                                                                                                                                    US-09-287-849-42
                    SEQ ID NO 62
LENGTH: 8
                                                                                                                                                                                                                     Matches
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                                                                                                                                    FEATURE:
NAME/KEY: misc feature
LOCATION: (6)...(6)
OTHER INFORMATION: The 'Xaa' at location 6 stands for Ser.
FEATURE:
OTHER INFORMATION: PCR primer: 508G
                                                                                                                                                                                                                                                                                                   54.1%; Score 33; DB 14; Length 8; 71.4%; Pred. No. 1.3e+06;
                                                                                                                                                                                                                                                                                                                                         2; Indels
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Publication No. US20050074785A1
GENERAL INPORMATION:
APPLICANT: Wood, Keith V.
APPLICANT: Hartnett, James Robert
APPLICANT: Promega Corporation
TITLE OF INVENTION: Vectors for Directional
FILE REFERENCE: 341.030US1
CURRENT APPLICATION WUMBER: US/10/702,228A
CURRENT APPLICATION NUMBER: US/204011-05
PRIOR APPLICATION NUMBER: 10/678,961
PRIOR PELICATION NUMBER: 10/678,961
PRIOR PELICATION NUMBER: 10/678,961
PRIOR FILING DATE: 2003-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 62. Application US/10678961B
Fublication No. US20050074883A1
GENERAL INFORMATION:
APPLICANT: Strauss, Ethan Edward
APPLICANT: Strauss, Ethan Edward
APPLICANT: Hartnett, James Robert
APPLICANT: Promega Corporation
TILLE OF INVENTION: Vectors for Directional Cloning
FILE REFERENCE: 341.023US1
CURRENT APPLICATION NUMBER: US/10/678,961B
CURRENT FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FRSEEQ ID NOS: 91
                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: A synthetic peptide
US-10-678-961B-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                  NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
  PRIOR FILING DATE: 1994-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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Matches 5; Conservative
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US-10-678-961B-62
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LENGTH: 8
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                                                                              LENGTH:
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Mark
APPLICANT: Campos-Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REPRENCE: 014058-0092003
CURRENT FILING DATE: 1999-04-07
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                                                                                                                                                 Length
                                                                                                                                                                                                 Indels
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                                                                                                                                            Score 31.5; DB 17;
Pred. No. 1.3e+06;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR PLING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-14
PRIOR PELING DATE: 1998-02-18
PRIOR PLING DATE: 1998-04-07
PRIOR PLING DATE: 1998-04-07
PRIOR PLING DATE: 1998-12-30
PRIOR PLING DATE: 1998-12-30
PRIOR PLING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 42
TYPE: PRT
COGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: A synthetic peptide
US-10-702-228A-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42, Application US/10359460; Publication No. US20030147911A1; GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 42, Application US/09287849
Patent No. US20020009459A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                         GENERAL INFORMATION
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: England Tool Tool
FILE OF INVENTION: 104058-00302003
CURRENT APPLICATION NUMBER: US/09/287,849
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR PRILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR PRILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 42
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APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE CANTE CORIXA CORPORATION
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009010US
CURRENT APPLICATION NUMBER: US/10/359, 459
CURRENT PILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence:flexible; OTHER INFORMATION: polylinker
US-10-359-460-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:flexible infoRMMATION: polylinker US-10-359-459-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.2%; Score 30; DB 15; Length 6; 80.0%; Pred. No. 1.38+06; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.2%; Score 30; DB 14; Length 6; 80.0%; Pred. No. 1.3e+06; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 6, Application US/10359459; Publication No. US20040013677A1; GENERAL INFORMATION: APPLICANT: Skeiky, Yasir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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Search completed: May 19, 2005, 18:19:58 Job time : 90.5 secs

us-09-867-159a-3.closed.rapb

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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May 19, 2005, 17:53:34 ; Search time 29.5 Seconds (without alignments) 25.305 Million cell updates/sec
OM protein - protein search, using sw model
                                                      Run on:
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US-09-867-159A-3 61 1 RMQGGCGSCN 10 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 segs, 74649064 residues Searched:

Total number of hits satisfying chosen parameters:

115750

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued Patents AA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	Sequence 59, Appl		62,	94,	Sequence 7, Appli	43,	m	'n	9	93	9	42,	7,	36,	7, 1	9, 2	57,	57,	57,	8, 7	θ,	Sequence 8, Appli	θ,	8	~	52,	52,
SUMMAKIES	ΩI	US-09-144-991B-59	US-09-144-991B-60	US-09-144-991B-62	US-09-470-191-94	US-09-223-040-7	US-09-287-849-43	US-08-835-099A-3	US-09-157-349-3	US-08-779-072A-6	US-09-470-191-93	US-09-223-040-6	US-09-287-849-42	US-08-779-072A-1	US-08-361-864-36	US-08-902-367-7	US-08-535-170-9	US-09-139-802-57	US-09-659-786-57	US-08-926-914-57	US-08-482-880-8	US-08-273-274-8	US-08-475-041-8	US-08-484-773-8	US-08-335-832-8	US-09-141-127-2	-69-	US-09-659-786-52
	DB	4	4	4	4	4	4	~	m	m	4	4	4	m	7	7	m	ო	4	4	٦	~	7	~	~	ო	m	4
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op.	Query	59.0	59.0	59.0	59.0	59.0	59.0	50.8	50.8	50.8	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5
	Score	36	36	36	36	36	36	31	31	31	30	30	30	30	30	30	30	30	30	30	29	29	29			29		29
	Result No.	1	~	m	4	S	9	7	σ0	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

52 100, 1111, 123, 133, 100, 110,	Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl
4 US-08-926-914-52 1 US-08-467-607-10 2 US-08-469-362-10 2 US-08-952-10 4 US-09-982-704-9 3 US-09-598-062-11 4 US-09-598-062-11 1 US-08-526-710-28 1 US-08-526-710-28 3 US-09-227-906-28 4 US-09-227-906-28 3 US-09-228-866-28 4 US-08-997-802-11 3 US-08-997-802-11	3 US-09-139-802-32 4 US-09-659-786-32 4 US-08-926-914-32
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2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 2 4 7

# ALIGNMENTS

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APPLICANT: BODOR, Nicholas Stephen
APPLICANT: BODOR, Nicholas Stephen
APPLICANT: BARTOLOMEO, Maria
TITLE OF INVENTION: COMPOUNDS AND METHOD FOR THE PREVENTION AND TREATMENT
TITLE OF INVENTION: OP IDABETIC RETINOPATHY
FILE REFERENCE: 028724-109
CURRENT APPLICATION NUMBER: US/09/144,991B
CURRENT APPLICATION NUMBER: US 60/058,423
PRIOR PILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cysteine residues at positions 3 and 6 are attached by a non-peptidal disulfide bond. Description of Unknown Organism:peptide derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid 1 is attached by Trig.
US-09-144-991B-59; Sequence 59, Application US/09144991B; Sequence 59, Application US/09144991B; Setent INFORMATION:
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83.3%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEX: BINDING
LOCATION: (1)
OTHER INFORMATION: A
NAME/KEX: BINDING
LOCATION: (7)
OTHER INFORMATION: A
OTHER INFORMATION: C
OCHER INFORMATION: C
OTHER INFORMATION: C
OTHER INFORMATION: C
OTHER INFORMATION: D
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                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Unknown
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-144-991B-59
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US-09-144-991B-60
Sequence 60, Application US/09144991B
Patent No. 6440933
GENERAL INFORMATION:
APPLICANT: BODOR, Nicholas Stephen;
APPLICANT: BARTOLOMEO, Maria 1 GGCGGC RESULT 2 셤

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6 255255
                                                                          1 GGCGGC 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-470-191-94
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US-09-223-040-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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Sequence 62, Application US/09144991B

Patent No. 644033

GENERAL INFORMATION:

APPLICANT: BODOR, Nicholas Stephen

APPLICANT: BARTOLOMEO, Maria

TITLE OF INVENTION: COMPOUNDS AND METHOD FOR THE PREVENTION AND TREATMENT

TITLE OF INVENTION: OF DIABETIC RETINOPATHY

FILE REFERENCE: 0.28724-109

CURRENT APPLICATION NUMBER: US/09/144,991B

CURRENT FILING DATE: 1998-09-01

PRIOR FILING DATE: 1997-09-10

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Patentin Ver. 2.0

LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
TITLE OF INVENTION: COMPOUNDS AND METHOD FOR THE PREVENTION AND TREATMENT TITLE OF INVENTION: OF DIABETIC RETINOPATHY
FILE REFERENCE: 028724-109
CURRENT APPLICATION NUMBER: US/09/144,991B
PRIOR APPLICATION NUMBER: US 60/058,423
PRIOR FILING DATE: 1999-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (3)..(6)
OTHER INFORMATION: Cysteine residues at positions 3 and 6 are
OTHER INFORMATION: attached by a non-peptidal disulfide bond.
OTHER INFORMATION: Description of Unknown Organism:peptide derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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COTHER INFORMATION: Cysteine residues at positions 3 and 6 are
OTHER INFORMATION: attached by a non-peptidal disulfide bond.
OTHER INFORMATION: Description of Unknown Organism:peptide derivative
                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (7)
OTHER INFORMATION: Amino acid 7 is attached by a hydroxide bond.
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OTHER INFORMATION: Amino acid 7 is attached by a hydroxide bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.0%; Score 36; DB 4; Length 7; 83.3%; Pred. No. 4.1e+05; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)
OTHER INFORMATION: Amino acid 1 is attached by Nic.
NAME/KEY: BINDING
                                                                                                                                                                                                                                                                                                                NAME/KEY: BINDING
COCATION: (1)
OTHER INFORMATION: Amino acid 1 is attached by Nic.
NAME/KEY: BINDING
                                                                                                                                                         NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3.,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: DISULFIDE LOCATION: (3)..(6)
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                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-144-991B-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-144-991B-62
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                                                                                                                                                                                                       SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                               FEATURE:
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Gaps

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Query Match 59.0%; Score 36; DB 4; Length 7; Best Local Similarity 83.3%; Pred. No. 4.1e+05; Matches 5; Conservative 0; Mismatches 1; Indels

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GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Composition and Methods of Their Use in
TITLE OF INVENTION: the Treatment, Prevention and Diagnosis of Tuberculosis
FILE REFERENCE: 014058-008910US
CURRENT APPLICATION NUMBER: US/09/470,191
CURRENT FILING DATE: 1999-12-23
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 94
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Skeiky, Yaair
APPLICANT: Skeiky, Yaair
APPLICANT: Alderson, Mark
APPLICANT: Campos-Netc, Antonio
APPLICANT: Campos-Netc, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Pusion Proteins of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: 10459-009010US
CURRENT APPLICATION NUMBER: US/09/223,040
CURRENT APPLICATION NUMBER: US/09/223,040
SOFTWARE: PATE: 1998-12-30
SOFTWARE: Patentin Ver. 2.1
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 4; Length 9; Pred. No. 4.1e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 59.0%; Score 36; DB 4; Length 9; Best Local Similarity 83.3%; Pred. No. 4.1e+05; Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: flexible polylinker
US-09-470-191-94
; Sequence 94, Application US/09470191
; Patent No. 6465633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09223040
Patent No. 6544522
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 59.0%;
Similarity 83.3%;
5; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GGCGSC 9
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STATE: M. COUNTRY:
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                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reed, Seeven G.
APPLICANT: Reed, Seeven G.
APPLICANT: APPLICANT: A.W.
APPLICANT: ALCANT: Corixa Corporation
TITLE OF INVENTION: Paid on Protients of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: And Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US 08/09/287, 849
CURRENT PILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/92,578
PRIOR PILING DATE: 1999-01-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SCOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-835-099A-3
; Sequence 3, Application US/08835099A
; Sequence 3, Application US/08835099A
; Patent No. S874277
; GENERAL INFORMATION:
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: KAWANTON: Tomohiro
; TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
; TITLE OF INVENTION: AND USE
; NUMBER OF SEQUENCES: 1
; ADDRESSE: ADDRESS:
; ADDRESSE: ADDRESS:
; STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 4; Length 9;
Pred. No. 4.1e+05;
0; Mismatches 1; Indels
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COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,099A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
                    Sequence 43, Application US/09287849
Patent No. 6627198
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 5; Conservative
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JS-09-287-849-43
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APPLICANT: SHINTANI, Yasushi
APPLICANT: SHINTANI, Yasushi
APPLICANT: NISHI, KAZINOTI
APPLICANT: NISHI, KAZINOTI
APPLICANT: KAWAMOTO, Tomohiro
TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 18
CORRESPONDENCES: 18
CORRESPONDENCES: ARDNESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 2; I
Pred. No. 4.1e+05;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
COMPUTER: IBM COMpatible
COMPUTER: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
FILLING DATE:
FILLING DATE:
APPLICATION NUMBER: 083649/1996
FILING DATE: 05-ARR-1996
APPLICATION NUMBER: 97105508.2
FILING DATE: 03-ARR-1997
ATORNEY/AGENT INFORMATION:
NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47342
TELEPHONE: 617-523-3400
TELEFAX: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/835,099
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S
REGISCRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09157349
Patent No. 6068990
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TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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FEATURE:
, OTHER INFORMATION: flexible polylinker
US-09-470-191-93
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Patent No. 6544522
                     APPLICANT: Skeiky, Yasir
APPLICANT: Corixa Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Ver. 2.1
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Best Local Similarity 80.0
Matches 4; Conservative
   GENERAL INFORMATION:
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SEQ ID NO 6
LENGTH: 6
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                                                                                                                                 Score 31; DB 3; Length 8;
Pred. No. 4.1e+05;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wickstrom, Eroc
APPLICANT: Basu, Soumitra
TITLE OF INVENTION: PEPTIDE NUCLEIC ACID CONJUGATES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Suite 1800, Two Penn Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31; DB 3; I
Pred. No. 4.1e+05;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.

ZIP: 19102
ZIP: 19102
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,072A
FILING DATE: January 7, 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/009,747
FILING DATE: January 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: MODACO, Daniel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MODACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-8383
TELEFX: (215) 568-8383
TELEFX: (215) 568-8383
TELEX: NO 61807676
TELEX: NO 61807676
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08779072A; Patent No. 6180767; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-470-191-93
; Sequence 93, Application US/09470191
; Patent No. 6465633
                                                                                                                                 50.8%;
                                                                                                                               Query Match 50.8
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
   8 amino acids
                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-779-072A-6
                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                           3 QGGCGSC 9
                                                                                                                                                                                                                                             OGGLGDC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GGCAAC 8
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                                                                                                                                                                                                                                                                                                  RESULT 9
US-08-779-072A-6
                                                                                          US-09-157-349-3
LENGTH:
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APPLICANT: COTIAN CORPORATION
TITLE OF INVENTION: Compositions and Methods of Their Use in
TITLE OF INVENTION: the Treatment, Prevention and Diagnosis of Tuberculosis
TITLE OF INVENTION: the Treatment, Prevention and Diagnosis of Tuberculosis
CURRENT ERFERENCE: 014058-008910US
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113,952
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 93
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009010US
CURRENT APPLICATION NUMBER: US/09/223,040
CURRENT APPLICATION NOS: 1098-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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OTHER INFORMATION: Description of Artificial Sequence:flexible
OTHER INFORMATION: polylinker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.2%; Score 30; DB 4; Length 6; 80.0%; Pred. No. 4.1e+05; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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49.2%; Score 30; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels
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US-09-287-649-42
US-09-287-649-42
; Sequence 42, Application US/09287849
; Patent No. 6627198
; GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Alderson, Mark
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
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Similarity 66.7%;
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
       SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 6.8
OTHER INFORMATION: /
OTHER INFORMATION: /
OTHER INFORMATION: i
                                                                                                : TOPOLOGY: linear
US-08-779-072A-1
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                      4 GGCGSC 9
                                                                                                                                                                                                                                                                                                        3 GGCSKC 8
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                                                                                                                                                                                                                                                                                                                                                                                               JS-08-361-864-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'EATURE:
                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                             ð
HAPLICANT: Corixa Corporation

TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REPERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT PILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR PELICATION NUMBER: US 08/818,112
PRIOR PELICATION NUMBER: US 08/942,578
PRIOR PELICATION NUMBER: US 09/025,197
PRIOR PELICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR PILING DATE: 1998-12-30
NUMBER OF SEQ 1D NOS: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence:flexible OTHER INFORMATION: polylinker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.2%; Score 30; DB 4; Length 6; 80.0%; Pred. No. 4.1e+05; 1:ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Basu, Soumitra
TITE OF INVENTION: PEPTIDE NUCLEIC ACID CONJUGATES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STRETE: Suite 1800, Two Penn Center Plaza
CITY: Philadelphia
STRATE: Pennsylvania
COUNTY: U.S.A.
ZIP: 1910
COMPUTER: BMR PA'S.
COMPUTER: MORGHERIEF FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KD
COMPUTER: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,072A
FILING DATE: January 7, 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/009,747
FILING DATE: January 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: MORGO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Monaco, Daniel A. REGISTRATION NUMBER: 30,480 REFERENCE/DOCKET NUMBER: 8321-14 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08779072A Patent No. 6180767 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: (215) 568-5549
TELEX: No. 6180767e
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e oseces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCGGC 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-779-072A-1
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 42
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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OTHER INFORMATION: /label= D-Tyr
OTHER INFORMATION: /note= "The tyrosine residue is in the D-stereo-
OTHER INFORMATION: chemical configuration"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site
LOCATION: 8..10
OTHER INFORMATION: /label= Tc-99m-chelator
OTHER INFORMATION: /note= "The sidechain sulfur atoms of both Cys
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Cyclic
/note= "The sidechain sulfur of the Cys
residue is covalently linked to the amino
terminus by a -CH2CO- group."
                                                                                          ö
                                             49.2%; Score 30; DB 2; Length 10; 57.1%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08902367
Patent No. 5997845
GENERAL INFORMATION:
APPLICANT: Dean, Nichard T.
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
ITILE OF INVENTION: Radiolabeled Compounds for Thrombus
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIALE: ILLINOIS
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,367
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive Seventh Floor
                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,668
PILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. 5997845nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-W
TELECHONE: 312 913 0001
TELECHONE: 312 913 0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: Modified-site
LOCATION: 1.5
OTHER INFORMATION: /label-
OTHER INFORMATION: /note=
OTHER INFORMATION: residue
OTHER INFORMATION: residue
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site LOCATION: 1..3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMAȚION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 300 South
CITY: Chicago
STATE: Illinois
                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                   3 QGGCGSC 9
                                                                                                                                                              2 RGDCGGC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
US-08-361-864-36
                                                                                                                                                                                                                                             RESULT 15
US-08-902-367-7
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CTHER INFORMATION: residues are each protected with an cutamic correct in the control of contr
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 19, 2005, 17:50:19 ; Search time 12 Seconds (without alignments) 80.181 Million cell updates/sec

US-09-867-159A-4 55 1 QPNYHAVNIV 10 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

1102 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
7	18	32.7	10	7	865387	cytochrome-c oxida
2	17	30.9	80	7	JS0316	leucokinin VI - Ma
٣	16	29.1	7	-	NY PG7	hypothalamic hepta
4	16	29.1	ď	~	PT0285	Ig heavy chain CRD
S	16	29.1	6	~	855696	phosphoenolpyruvat
9	16	29.1	10	~	A43405	6-phosphofructo-2-
7	16	29.1	10	7	S33844	alpha-2-macroglobu
8	16	29.1	10	7	PT0291	Ig heavy chain CRD
6	16	29.1	10	N	A59272	peptide-N4- (N-acet
10	16	29.1	10	~	S23307	neurokinin A - rai
11	16	29.1	10	N	S23186	neurokinin A - Atl
12	15	27.3	7	~	A38081	amine oxidase (cop
13	15	27.3	7	N	A15398	choline oxidase (E
14	15	27.3	ω	~	A44960	neuropeptide Led-C
15	15	27.3	80	~	B44960	neuropeptide Led-C
16	15	27.3	ω	7	808995	hypertrehalosemic
17	15	27.3	œ	~	966808	hypertrehalosemic
18	15	27.3	ω	7	A49823	adipokinetic hormo
19	15	27.3	œ	~	B49823	adipokinetic hormo
20	15	27.3	80	~	S15422	adipokinetic hormo
21	15	27.3	œ	~	A43976	hypertrehalosemic
22	15	27.3	68	~	B43976	hypertrehalosemic
23	15	27.3	60	~	A58641	adipokinetic hormo
24	15	27.3	œ	~	A05169	neuropeptide M-I
25	15	27.3	6	~	S70345	amine oxidase (cop
26	15	27.3	o,	~	PT0270	Ig heavy chain CRD
27	15	27.3	თ	~	S13889	phosphoenolpyruvat
28	15	27.3	თ	N	S77984	Š
29	15	27.3	10	Ч	ECLQ4M	tachykinin IV - mi

RESULT 2

Jeucokinin VI - Madeira cockroach
Cispecies: Leucophaea maderae (Madeira cockroach)
Cispecies: Leucophaea maderae (Madeira cockroach)
Cispecies: Leucophaea maderae (Madeira cockroach)
Cispace: Of-Sep-1990 #sequence_revision O7-Sep-1990 #text_change 09-Jul-2004
Cispacesolon: JS0316
R.Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A.Fitle: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic, A.Fitle: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic, A.Fitle: Isolation, Drotein
A.Residues: 1-8 <-HOL>
A.Fitle: Leucokinins V as family of cephalomyotropic peptides, stimulate contractile act Cicoment: Leucokinins, a family of cephalomyotropic peptide; pyroglutamic acid Cikeywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid F://Modified site: pyrrolidone carboxylic acid (GIn) #status experimental

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Gaps ö

Query Match
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 1; Indels

hypertrehalosemic hypertrehalosemic	1-cell receptor al hypothetical 1.3K angiotensin-conver	glutathione transf MHC class I histoc	photosystem II pro Ig heavy chain CRD	Ig heavy chain CRD calliFMRFamide 4 - inhibin beta-A cha	in C -	dermorphin (Trp-4,
JC1416 S09138	F10213 JQ0943 PQ0008	S71867 A59028	A1123 C41170 PT0288	PT0324 D41978 S10926	A60647 A44916	S21230
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100	101	V 80	י טיטי	000	10	7
27.3	27.3 25.5	25.5	25.5	25.5 25.5 25.5	25.5	23.6
15	15 14	444	1 1 1 1	4 4 4	14	13
30	3 3 2	3 9 2	8 6 6 8 6 6	4 4 4 0 1 2	4 4	45

# ALIGNMENTS

RESULT 1			
S65387			
cytochrome-c oxidase (EC 1.9.3.1) chain VII b, cardiac - rat (fragment)	(fragment)		
C;Species: Rattus norvegicus (Norway rat)			
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004	nge 09-Jul-	.2004	
C;Accession: S65387; S65386 _			
R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.	λw, G.		
Eur. J. Biochem. 230, 235-241, 1995			
A, Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term	c properti	es and amino-t	term
A; Reference number: S65372; MUID:95324529; PMID:7601105			
A; Accession: S65387			
A;Status: preliminary			
A;Molecule type: protein			
A; Residues: 1-10 <sch></sch>			
A; Cross-references: UNIPROT: P80431			
A; Accession: S65386			
A;Status: preliminary			
A; Molecule type: protein			
A;Residues: 1-10 <sc2></sc2>			
C;Keywords: cardiac muscle; heart; oxidoreductase			
Query Match 32.7%; Score 18; DB 2; Length 10;			
Best Local Similarity 50.0%; Pred. No. 1.6e+03;			
Matches 2; Conservative 1; Mismatches 1; Indels	з 0; Сарв	, 0 sq	
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Db 7 PTFH 10			

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29.1%;
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Matches 3; Conservative
                                                    3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein A; Residues: 1-10 < WAR>
Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-10 < YAM>
                                                                                            1 QPNYH 5
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                                                                                                                                     1 QPIIH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 OVNOH 5
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Matches
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$55696
phosphoenolpyruvate carboxykinase - Trypanosoma brucei
c;Species: Trypanosoma brucei
c;Species: Trypanosoma brucei
c;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
c;Accession: 555696
R;Hunt, M.; Koehler, P.
Biochim. Biophys. Acta 1249, 15-22, 1995
A;Titles: Purification and characterization of phosphoenolpyruvate carboxykinase from Try
A;Reference number: 555696; MUID:95284106; PMID:7766679
                                                                                                                                                                         hypothalamic heptapeptide - pig (Species: Sus acrofa domestic pig)
C;Species: Sus acrofa domestica (domestic pig)
C;Species: Ol-Sep-1981 #sequence_revision Ol-Sep-1981 #text_change 09-Jul-2004
C;Accession: A01417
C;Accession: A01417
R;Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong, Horm. Metab. Res. 13, 228-232, 1981
A;Tile: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-releasi A;Reference number: A01417; MUD: 81213980; PMID: 6263778
A;Accession: A01417
A;Accession: A01417
A;Residues: 1-7 <CHA>
A;Cross-references: UNIPROT:P01153
C;Superfamily: hypothalamic heptapeptide
C;Keywords: hypothalamus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain CRD3 region (clone 4-100A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0285
I; Accession: PT0285
I; Exp. Med: 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102
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Pred. No. 2.8e+05;
1; Mismatches 1;
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A;Molecule type: DNA
A;Residues: 1-9 < YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
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Best Local Similarity 50.00,
1.00 2; Conservative
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Best Local Similarity 66.7
Matches 2; Conservative
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A;Molecule type: protein
A;Residues: 1-9 <HUN>
                             OPNYHA 6
                                                    OSSFHS 6
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PTYY 7
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6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2,6-bisphosphate 2-phosphatase (EC 3.3 C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: A43405
R;Ventura, F:; Rosa, J.L.; Ambrosio, S.; Pilkis, S.J.; Bartrons, R.
J. Biol. Chem. 267, 17939-17943, 1992
A;Title: Bovine brain 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase. Evidence for A;Reference number: A43405; MUID:92388154; PMID:1325453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: A43405
A,Molecule type: protein
A,Residues: 1-10 <VEN>
A,Cross-references: UNIPROT:Q7M313
C,Superfamily: 6-phosphofructo-2-kinase / fructose-2,6-bisphosphate 2-phosphatase; phospł
C,Suporfamily: 6-phosphofructo-10-kinase / fructose-2,6-bisphosphate 2-phosphatase; phospł
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-2-macroglobulin - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: S33844
R;Warburton, M.J.; Coles, B.; Dundas, S.R.; Gusterson, B.A.; O'Hare, M.J.
Bur. J Blochem. 214, 803, 1993
A;Fitle: Hydrocortisone induces the synthesis of alpha(2)-macroglobulin by rat mammary my. A;Reference number: S33843; MUID:93307297; PMID:7686489
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A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jc A;Reference number: PT0222; MUID:91108337; PMID:1899102
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0291
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C;Keywords: glycoprotein; plasma; proteinase inhibitor; thiolester bond
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Score 16; DB 2; Length 9; Pred. No. 2.8e+05; 0; Mismatches 2; Indels
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Pred. No. 3.8e+03;
0; Mismatches 2; Indels
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A.Molecule type: protein
A.Residues: 1-10 <JEN>
A.Cross-references: UNIPROT:P28500
A.Experimental source: brain
C.Function: may play a physiological role in the regulation of cardiovascular and gass.
A.Description: may play a physiological role in the regulation of preprotachykinin A A.Note: neuropeptide, amidated by post-translational processing of preprotachykinin A C.Keywords: neuropeptide, amidated carboxyl end, tachykinin
F;10/Modified site: amidated carboxyl end (Met) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Pichia angusta
C; Species: Pichia angusta
C; Jate: 31.Dec.1993 #sequence_revision 03-Feb-1994 #text_change 20-Apr-2000
C; Accession: A38081
R; Mu, D.; Janes, S.M.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Klinman, J.P.
R; Mu, D.; Janes, S.M.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Klinman, J.P.
A; Biol. Chem. 257, 7979-7982, 1992
A; Title: Tyrosine codon corresponds to topa quinone at the active site of copper amine os A; Reference number: A38081; MUID:92235001; PMID:1569055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Ohta-Fukuyama, M.; Miyake, Y.; Emi, S.; Yamano, T.
Biocham. 88, 197-203, 1980
A;Title: Identification, and properties of the prosthetic group of choline oxidase from Al
A;Reference number: A15398; MUID:81006769; PMID:6997283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amine oxidase (copper-containing) (EC 1.4.3.6) - yeast (Pichia angusta) (fragment)
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C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A15398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.3%; Score 15; DB 2; Length 7; 60.0%; Pred. No. 2.8e+05; Live 0; Mismatches 2; Indels
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A;Residues: 1-7 <MUA>
C;Keywords: copper, copper, copper, quinoprotein; topaquinone
C;Keywords: copper; copaquinone (Tyr) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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A;Reference number: S23186; MUID:92298992; PMID:1376687
A;Accession: S23186
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C, Keywords: oxidoreductase
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Best Local Similarity
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1 HKIN 4
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523186
6.
523186
C.Species: Gadus morbua (Atlantic cod)
C.Species: Gadus morbua (Atlantic cod)
C.Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C.Accession: 523186
C.Accession: 523186
C.Accession: 523186
C.Accession: 52086
C.Accession: 520
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C;Species: Oncorhynchus mykiss (rainbow trout)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C;Accession: 523307
R;Jensen, J.; Conlon, J.M.
Eur. J. Blochem. 206, 659-664, 1992
A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod A;Reference number: 523186; MUID:92298992; PMID:1376687
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A59272

Beptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (BC 3.5.1.52) A, large chain N,Alternate names: peptide N-glycosidase
C;Species: Prunus dulcis var. sativa (sweet almond)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A59272
R;Altenann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
Eur. J. Biochem. 252, 118-123, 1998
A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A;Reference number: A59272; MUID:98181894; PMID:9523720
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                                                                                                            Score 16; DB 2; Length 10;
Pred. No. 3.8e+03;
1; Mismatches 1; Indels
   A; Experimental source: B lymphocyte C; Keywords: heterotetramer; immunoglobulin
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A;Molecule type: protein
A;Residues: 1-10 <JEN>
A;Cross-references: UNIPROT:P28500
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C; Keywords: hydrolase
                                                                                                        Query Match 29.1%;
Best Local Similarity 50.0%;
Matches 2; Conservative
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A;Molecule type: protein
A;Residues: 1-10 <ALT>
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neuropeptide Led-CC-I - Colorado potato beetle
C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
C;Species: Lostinotarsa decemlineata (Colorado potato beetle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A44560
R;Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and A;Reference number: A44960, MUID:90160053; PMID:2576128
A;Accession: A44960
A;References: UNIPROT:P04548
A;Cross-references: UNIPROT:P04548
C;Superfamily: adipokinetic hormone
C;Superfamily: hormon
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Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0;
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RESULT 15
B44960
neuropeptide Led-CC-II - Colorado potato beetle
C;Species: Leptinotarsa decemineata (Colorado potato beetle)
C;Species: Leptinotarsa decemineata (Colorado potato beetle)
C;Species: 10-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: 844960
R;Gaade, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and A;Reference number: A44960; MUID:90160053; PMID:2576128
A;Reference number: A44960; MUID:90160053; PMID:2576128
A;Residues: 1-8 cGAE>
A;Cross-references: UNIPROT:P04549
C;Superfamily: adipokinetic hormone
C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic C;Keywords: blocked carboxyl end (Trp) (probably amidated) #status experimental
F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

ö Gaps ö Ouery Match 27.3%; Score 15; DB 2; Length 8; Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 0; Indels

2 PNY 4 ઠે

6 PNW 8 셤 Search completed: May 19, 2005, 17:59:35 Job time : 14 secs

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Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V., Schiffmann E., Liotta L.A.;
"Identification, purification, and partial sequence analysis of autotaxin, a novel motility-stimulating protein.";
J. Biol. Chem. 267:2524-2529(1992).
GO: 0006928; P:cell motility; NAS.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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STRAIN=PV6/95, and PV7/95;

MEDLINE=22838663; PubMed=12958242;

Hard M., Del Aguila C., Fenoy S., Henriques-Gil N.;

Intramperies genotype variability of the microsporidian parasite Encephalitozoon hellem.";

J. Clin. Microbiol. 41:4166-4171 (2003).

EMBL; AY171238; AAN73415.1;

EMBL; AY171239; AAN73417.1;

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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NCBI _TaxID=27973;
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01-MAR-2003 (TrEMBLrel. 23,
05-JUL-2004 (TrEMBLrel. 27,
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ilarity 57.1%;
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Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                     Serratia plymuthica.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Serratia.
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32.7%; Score 18; DB 1; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.6e+06;
Matches 2; Conservative 3; Mismatches 2; Indels
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibiotic; Bacteriocin; Direct protein sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AA; 981 MW; 293E01E865A776D8 CRC64;
                                                                                                                                      9 A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AML1 protein (Fragment)
Name=AML1;
       3 NYHAVNIV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                    2 NDHFVKLV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 YHAVNIV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 HHGVRVL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=82996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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NON TER
SEQUENCE
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Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Scincomorpha, Scincoidea,
Scincidae, Carlia.
NCBI_TaxIb=260893;
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Dolman G., Phillips B.;
Wingle copy nuclear DNA markers characterized for comparative phylogeography in Australian wet tropics rainforest skinks.";
Mol. Ecol. Notes 4:185-187(2004).
EMBL, AYSO8912; AASO9890.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 34.5%; Score 19; DB 2; Length 10; Best Local Similarity 50.0%; Pred. No. 5.9e+03; Matches 4; Conservative 1; Mismatches 3; Indels
                                                                                             Score 20; DB 2; Length 10;
Pred. No. 3.7e+03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.5%; Score 19; DB 2; Length 9; 42.9%; Pred. No. 1.6e+06; ative 1; Mismatches 3; Indels
       1 1
10 10
10 AA, 1171 MW, 736F44577AF1B2CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AA; 1171 MW; 9D0ABB2322C9C1EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polyprotein.
1 1 SEQÜENCE 9 AA; 1177 MW; C40404473401F1B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Glyceraldehyde-3-phosphate dehydrogenase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                            36.4%; Scor.
100.0%; Pred. No. ...
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Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                     Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polyprotein (Fragment).
Barley mild mosaic virus.
                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=12466;
                                                                                                                                                                                         2 PNY 4
                                                                                                                                                                                                                                    7 PNY 9
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Carlia zuma
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                                                                                                Query Match
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QGR7V4
AC GGR7
AC GGR7
DD 05-J
DT 05-
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C68E32486AF77B46 CRC64;
GO; GO:0005618; C:cell wall; IEA.
Cell wall.
NON II
SEQÜENCE 10 AA; 1126 MW; C68E
                                                        h 32.7%;
Similarity 37.5%;
3; Conservative
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                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                               SEQUENCE, AND SYNTHESIS.
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                                                                                                                                                                                                                                                        Panagrellus redivivus
                                                                                                      2 PNYHAVNI 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                         Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                            POYPXGNV
                                                                                                                                                                                                                                                                                           NCBI_TaxID=6233;
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1 KPNF 4
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LCK6_LEUMA
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PANRE
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
50 kDa cell wall protein (Fragment).
Nicotiana tabacum (Common tobacco).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; asterids;
                                                                                                                                                                                                                                                                                                                                                  Carucci D.J.;
"Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                              PubMedillides, DOI=10.1038/nature01099;
Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
Silva J.C., Ermolaeva M.D., Allen J.E., Sebengut J.D., Koo H.L.,
Shallom S.J., van Aken S.E., Riedmuller S.B., Beldblyum T.V.,
Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. PETIT HAVANA, Mitchell G.P., Robertson D., Slabas A.R., Harbana V.A., Mitchell G.P., Robertson D., Slabas A.R., Wojtaszek P., Bolwell G.P., "Proteomic study of secondary cell wall proteins from transformed
                                                                                                                                                                                                                                                                                                                                                                        parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                           Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 2; Length 10;
Pred. No. 9.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data.
EMBL, AABLO1001270; EAA16068.1; -.
Hypothetical protein.
SEQUENCE 10 AA; 1332 MW; P8601A30545B5051 CRC64;
                                                                                                                  Last sequence update)
Last annotation update)
                                                                                 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lamiids; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;
                                                                                                        Created)
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                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                   32.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tobacco culture.";
Planta 0:0-0(2000)
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 YHAVNI 9
                                                                                                                                                                                   NCBI_TaxID=73239;
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                       OPSGH 7
    OPNYH
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                                                                                             Q7RGV8;
                                                                                 Q7RGV8
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                                                          RESULT 7
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P82438
                                                                      Q7RGV8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE-27052651; PubMed=2877794; DOI=10.1016/0742-8413(86)90077-0; HOlman G.M., Cook B.J., Nachman R.J.; "Isolation, primary structure, and synthesis of leucokinins V and VI:
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 muscle tension increase.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;
Neoptera, Orthopteroidea, Dictyoptera, Blattaria, Blaberoidea;
Score 18; DB 2; Length 10;
Pred. No. 9.3e+03;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.9%; Score 17; DB 1; Length 7; 50.0%; Pred. No. 1.6e+06; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
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Amidation; Direct protein sequencing; Neuropeptide.

MOD RES 7 7 Phenylalanine amide.

SEQÜENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
FMRFamide-like neuropeptide PF4 (KPNFIRF-amide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Panagrolaimoidea; Panagrolaimidae; Panagrellus
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01-FEB-1994 (Rel. 28, Last sequence update)
05-ULL-2004 (Rel. 44, Last annotation update)
Leucoxinin VI (L-VI).
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                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Envelope protein.
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P01153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8QE18
Q8QE18;
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         OSC OS BILLIAND
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                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                         -i- FUNCTION: This cephalomyotropic peptide stimulates contractile activity of cockroach protodeum (hindgut).
-i- SUBCELLULAR LOCATION: Secreted.
-i- SUBCELLULAR LOCATION: Secreted.
PIR; JS0316; JS0316.
Amidation; Direct protein sequencing; Neuropeptide;
Pyrrolidone carboxylic acid.
MOD_RS:
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cloce V., Schlffmann E., Liotta L.A.,
"Identification, purification, and partial sequence analysis of autotaxin, a novel motility-stimulating protein.";
G. Biol. Chem. 267:2524-2591(992).
GO: GO:0005576; C:extracellular; IDA.
GO; GO:0030334; P:regulation of cell migration; IDA.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Pred. No. 1.5e+04;
3; Mismatches 3; Indels
                                                                                                                                                                                                             1 1 Pyrrolidone carboxylic acid.
8 8 Glycine amide.
8 AA, 935 MW, 9D6365BlE9D5A5A6 CRC64;
                                                                                                                                                                                                                                                                                                                                          30.9%; Score 17; DB 1; Length 8; 33.3%; Pred. No. 1.6e+06;
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PubMed=12368865; DOI=10.1038/nature01099;
   Biochem. Physiol. 88C:27-30(1987)
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                                                                                                                                                                                                                                                                                                                                                                                                       2; Conservative
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PPFENINL 9
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SEQUENCE
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Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sadgah M., Shoaibi A., Cummings L.M., Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Carberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.

NCBI_TaxID=9823;
                                                                                                                                                                                                                   parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                  preliminary data.
EMBL, AABLO100104; EAA15335.1; -.
Hypochetical procein.
SEQUENCE 10 AA; 1279 MW; 11EBECB04B4B4B50 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
fruncated envelope glycoprotein (Fragment).
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Human immunodeficiency virus 1.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                MEDIINE=81213980; PubMed=6263778; Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H., Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.; Isolation, structure and synthesis of a heptapetide with in vitro ACTH-releasing activity from porcine hypothalamus."; Horm. Metab. Res. 13:228-232(1981).

PIR; A01417; NYPG7.

Direct protein sequencing.

SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;
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MEDLINE=96009872; PubMed=7557411; DOI=10.1016/0378-1119(95)00308-S;
Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.
Liras P.,
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29.1%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels
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Name=cefF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 66.7 tes 2; Conservative
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[1]
SEQUENCE, AND SYNTHESIS.
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YHS 5
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Search completed: May 19, 2005, 18:15:46 Job time : 115 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

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May 19, 2005, 17:47:19; Search time 141 Seconds (without alignments) 27.430 Million cell updates/sec

US-09-867-159A-4 55 1 OPNYHAVNIV 10 Perfect score:

Seguence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 seqs, 386760381 residues Searched:

465227 Total number of hits satisfying chosen parameters:

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geneseqp1980s:* geneseqp200s:* geneseqp200s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003as:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	no	Cysteine	Cysteine	House dus	House dus	Peptide d	Soybean p	Human Eph	Human pap	Human pap	Human pap		Human pap	Human BLy	SCFV VHCD	Human can	Human can	Human can	Human can	Hepatitis	Human can					
	Description	Aao20570	Abb98535	Abu11122	Abu11108	Aay23224	Aae10569	Ade85720	Adk09727	Adk09741	Adk09742	Adk09740	Adk09760	Abp46729	Adg97556	Abr 25375	Abr25590	Abr24431	Abr25198	Aar96521	Abr24938	Abr24674	Abr25279	Abr25474	Abr25523	Abr25760
COLUMNICO	ai .	AA020570	ABB98535	ABU11122	ABU11108	AAY23224	AAE10569	ADE85720	ADK09727	ADK09741	ADK09742	ADK09740	ADK09760	ABP46729	ADG97556	ABR25375	ABR25590	ABR24431	ABR25198	AAR96521	ABR24938	ABR24674	ABR25279	ABR25474	ABR25523	ABR25760
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ABR24521 ABR25108 ABR25710	AAU08238 ABB99503 ABG76122 ADR19346	AAR73741 AAR77563 ABU11107 ABD05547	ABR05672 ABR05873 ADR11486 AAP82560	ABR05590 ABR05041 ABR05844 ADO37899 ADO37682
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# ALIGNMENTS

AA020570

AAO20570 standard; peptide; 10 AA.

02-JAN-2003 (first entry)

Cysteine protease epitope peptide region, SEQ ID No 4.

Antiallergic; antiinflammatory; antiasthmatic; dermatological; allergen; anti-histamine; histamine synthesis inhibitor; allergic hypersensitivity; allergic asthma; allergic rhinitis; cysteine protease protein; enzyme; atopical eczema; epitope. 

Dermatophagoides pteronyssinus.

WO200278736-A2.

10-OCT-2002

28-MAR-2002; 2002WO-FR001098.

30-MAR-2001; 2001FR-00004370. 03-MAY-2001; 2001FR-0005929. 29-MAY-2001; 2001US-00867159.

(ANTI-) ANTIALIS SARL.

Terrasse G, Loria E,

WPI; 2002-750636/81.

Antiallergic compositions containing an anti-histamine, a histamine synthesis inhibitor, and optionally an allergen or nucleic acid coding for the allergen.

Claim 14; Page 11; 32pp; French.

The invention relates to antiallergic compositions containing an antihistamine, a histamine synthesis inhibitor, and optionally an allergen or isolated nucleic acid molecule that has at least one polymucleotide sequence coding for the allergen, together with a pharmaceutical carrier. The pharmaceutical composition of the invention is useful as a non-specific antiallergic treatment, and also useful in the treatment of allergic hypersensitivity, allergic asthma, allergic rhinitis, and allergic and acopical eczema. This sequence represents a peptide of a cysteine protease epitope region relating to the antiallergic

Matches

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The present invention relates to house dust mite (Dermatophagoides pteronyssinus) Der pl antigen peptides containing human CD8 cell epitopes. The peptides of the invention are useful in the treatment of human or animal patients, particularly to raise an immune response to the allergies to the major house dust mite antigen, and to monitor disease activity in atopic patients. ABULIO78-ABULI146 represent house dust mite of patients and prevention of ber pl antigen peptides containing CD8+ T-cell epitopes
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Dermatophagoides ptéronyssinus contain a human CD8+ T cell epitope ar
are useful to treat and prevent allergy to the major house dust mite
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                                                                                                                                                  House dust mite, Der pl antigen, human CD8 cell epitope, allergy,
immune response, atopic patient, CD8+ T-cell epitope, antiallergic.
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Pred. No.
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   ABU11122 standard; peptide; 9 AA.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to an antiallergic pharmaceutical composition (1) comprising a pharmaceutical carrier containing an active agent combination of at least two of: an allergen; an antihistamine; and a histamine synthesis inhibitor. (1) is used for treating or preventing allergic hypersensitivity reactions, especially allergic asthma, allergic thintis or allergic eczema, in babies, children or adults. The present sequence is a peptide fragment (epitope) of cysteine protease from Dermatophagoides pteronyssinus, which was used as an allergen in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antiallergic composition, useful for preventing and treating e.g. asthma, rhinitis or eczema, containing at least two of allergen, antihistamine and histamine synthesis inhibitor.
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compositions of the invention
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RESULT 3

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Strasser R,
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Steinkellner H;
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                                                                                                                                                                The present invention relates to house dust mite (Dermatophagoides pteronyssinus) Der plantigen peptides containing human CD8 cell epitopes. The peptides of the invention are useful in the treatment of human or animal patients, particularly to raise an immune response to the Der plantigen. They are useful in the treatment and prevention of altergies to the major house dust mite antigen, and to monitor disease activity in atopic patients. ABULIO78-ABULI146 represent house dust mite Der plantigen peptides containing CD8+ T-cell epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-1,2-xylosyltransfease; beta 1,2-linked xylose; beta-linked mannose; N-linked oligosaccharide; storage glycoprotein; allergenicity; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY23220-24 represent peptides released by beta-1,2-xylosyltransfease by Endo lys C digestion. The specification describes a plant-derived beta
                                                                                             New peptide fragments of the Der pl antigen of the house dust mite
Dermatophagoides pteronyssinus contain a human CD8+ T cell epitope and
are useful to treat and prevent allergy to the major house dust mite
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Pred. No. 1.8e+06;
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                                                                                                                                                Disclosure; Page 31; 47pp; English
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03-APR-2002; 2002WO-GB001534.
                   06-APR-2001; 2001GB-00008752.
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1,2-xylosyltransferase, where the enzyme adds a beta 1,2-linked xylose to the beta -linked mannose on the N-linked oligosaccharides of storage glycoproteins. Xylose units on N-linked oligosaccharides may play a critical role in allergenicity of plant derived glycoproteins and may also be important in regulating the structure of the oligosaccharide chains and the targeting of these proteins. Purification of a xylosyltransferase is useful in order to study its properties and specificities in the absence of interfering activities and possible inhibitors. The antibody can be used to determine the localization of the xylosyltransferase in suspension culture soybean cells and the distribution and level of the enzyme in plants as well as its levels at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to Arabidopsis thaliana beta 1,2-xylosyltransferase plant protein and its cDNA molecule. Beta 1,2-xylosyltransferase protein mucleic acid (PNA) molecule is useful for producing transgenic plants and plant cells with increased efficiency in producing glycoproteins. The invention also relates to a method for producing recombinant human glycoproteins which is suitable for medical use. Beta 1,2-xylosyltransferase DNA is useful for immobilisation on DNA microarrays, e.g. for finding homologous sequences or for expression studies in plants or non-vertebrate animals. The invention is also useful for inactivation, suppression or over expression and production of beta 1,2-xylosyltransferase. The present sequence is soybean peptide 3 which is used for analysing Arabidopsis thaliana beta 1,2-xylosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30; DB Pred. No. 34; 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE10569 standard; peptide; 8 AA.
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producing transgenic plants
producing glycoproteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 various stages of growth
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                                                                                                                            Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; hyperproliferative cell disease; EphA2 antibody; EphA2 agonistic antibody; cytostatic; antiasthmatic; antipsoriatic; antiflammatory; vasotropic; respiratory; gene therapy; metastatic cancer; asthma; psoriasis; inflammatory bowel disease; smooth muscle restenosis; endothelial restenosis; Crohn's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human EphA2 antibody Eph099B-233.152 VH CDR3 SEQ ID NO:24
                                                           Score 28; DB 4; Length 8;
Pred. No. 1.8e+06;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chronic obstructive pulmonary disease; human
                                                                                                                                                                                                                                                                                                                                                                                            ADE85720 standard; peptide; 9 AA.
                                                        50.9%;
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                                                                                                                         4; Conservative
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                                                           Query Match
Best Local Similarity
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Sequence 8 AA;
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                                                                                                                         Matches
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antipsoriatic, antiinflammatory, vasotropic and respiratory activities, and can be used in gene therapy. The composition and methods are useful in managing, diagnosing, preventing or treating hyperproliferative cell diseases (i.e. metastatic cancer) or non-cancer hyperproliferative cell diseases or disorders, such as asthma, psoriasis, inflammatory bowel disease, smooth muscle restenosis, endothelial restenosis, Crohn's disease or chronic obstructive pulmonary disease. They may also be used for monitoring the efficacy of therapy for cancer in a patient known to or suspected to have cancer, and in screening for anti-cancer drugs. The present sequence is used in the exemplification of the present invention.
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Pred. No. 1.8e+06;
2; Mismatches 1; Indels
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Pred. No. 1.8e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus peptide #1782.
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11-JUL-2003; 2003EP-00450171.
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Matches 4; Conservative
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2 PRYHAMD
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                                                                                                                                                                                                                                                                                                           Sequence 9 AA;
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Claim 54; SEQ ID NO 24; 173pp; English.

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Human papillomavirus peptide #1797.
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                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                             Schmidt W,
                                                                                                                                                          (INTE-) INTERCELL AG
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                                              Human papillomavirus
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                                                                    WO2004011650-A2
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                                                                                                                                                                                                                                                                                                                                                                       invention.
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                                                                                                                                                                                                                                                                                                                                                                    New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
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  1; Indels
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 0; Mismatches
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                                                                                                                                                Human papillomavirus peptide #1796.
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                                                                                      ADK09741 standard; peptide; 9 AA.
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4; Conservative
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                                                                                                                                                                                                Human papillomavirus
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                   1 QPNYH 5
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ADK09742
1D ADK09
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This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigionic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
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pathogenic virus; alternative reading frame; antigenic determinant; virucide; vaccine; therapeutic agent; infection; HPV.
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80.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 1;
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11-JUL-2003; 2003EP-00450171.
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11-JUL-2003; 2003EP-00450171
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This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antiganic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a
                                                                                                       New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogenic virus; alternative reading frame; antigenic determinant; virucide; vaccine; therapeutic agent; infection; HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         49.1%; Score 27; DB 8; Length 9; 80.0%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                     Claim 18; Page 193; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 193; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus peptide #1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADK09760 standard; peptide; 10 AA.
                                              Habel A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Habel A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUL-2003; 2003WO-EP008112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUL-2002; 2002AT-00001124
11-JUL-2003; 2003EP-00450171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mattner F, Schmidt W,
                                              Schmidt W,
                (INTE-) INTERCELL AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INTE-) INTERCELL AG
                                                                          WPI; 2004-169243/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-169243/16.
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 OPNYH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPRYH 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004011650-A2
                                                                                                                                                                                                                                                                                                                                                                           Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2004.
                                             Mattner F,
                                                                                                                                                                                                                                                                                                                                             invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADK09760;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Gaps

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methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel antibodies that immunospecifically bind to by Lymphocyte Stimulator (BLyS) polypeptides. BLyG is a member of the tumour necrosis factor (TMP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunosdulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so well as the detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                         Length 10;
                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hilbert D;
                                                                                                                                                                                                     Score 27; DB 8; I
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human BLyS binding acFv VH CDR3 SEQ ID 2740.
                                                                                                                                                                                                                                              . O. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 3042; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               ABP46729 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUN-2000; 2000US-0212210P.
17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
                                                                                                                                                                                                         49.1%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2001; 2001US-0293499P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                              4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-114799/15.
                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                    2 OPRYH 6
                                                                                                                                                                      Sequence 10 AA;
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                                                                                                                                                                                                                                                                                 1 QPNYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                   invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP46729;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                               늉
                                  diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
  expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to novel antibodies that immunospecifically bind
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B cell proliferation; differentiation; scrv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scFV VHCDR3 peptide that immunospecifically binds BLyS SeqID 2740.
administered to treat diseases associated with aberrant BLyS exprand activity such as cancer, immune, and autoimmune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
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                                                                                                                                                                                            Score 26; DB 5; Length 8;
Pred. No. 1.8e+06;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaughan TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 2740; 394pp; English.
                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                ADG97556 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-NOV-2001; 2001US-0331469P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-NOV-2002; 2002WO-US036496.
                                                                                                                                                                                              47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                               Similarity 37.8
3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-505530/47.
                                                                                                                                                                                                                                                                          PNYHAVNI 9
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PSYHYMDV 8
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                                                                                                                                                        Sequence 8 AA;
                                                                                                                   the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-2004
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                                                                                                                                                                                          Query Match
Best Local &
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                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in
lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiarthritic, neuroprotective, antialidammatory, antiallergic and cytostatic. This peptide sequence is a single chain antibody variable heavy CDR3 peptide that immunospecifically binds BLyS of the invention.
                                                                                                                                                                  Gaps
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                                                                                                                                                                1; Indels
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                                                                                                                                  Length
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                                                                                                                                Score 26; DB 7; I
Pred. No. 1.8e+06;
I; Mismatches 1;
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Pred. No. 1.8e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morrison RK, Raitano AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Page 380; 1021pp; English
                                                                                                                                                                                                                                                                                                              ABR25375 standard; peptide; 9 AA.
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25-APR-2001; 2001US-0286630P.
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                                                                                                                                Query Match
Best Local Similarity
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Best Local Similarity
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PSYHYMDV
                                                                                                                                                                                                2 PNYHAVNI
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                                                                                                  Sequence 8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                  Matches
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0; Gaps

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Matches 3; Conservative 4; Mismatches ò

2 PNYHAVNI 9 |::|: |: 2 PDFHSENL 9

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Search completed: May 19, 2005, 17:59:10 Job time : 146 secs

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May 19, 2005, 17:59:41 ; Search time 89.5 Seconds (without alignments) 37.375 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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55
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                                                                                                                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Sequence 4, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 24, Appl	Sequence 2740, Ap	Sequence 2740, Ap	Sequence 204, App	Sequence 162, App	Sequence 4, Appli	Sequence 4, Appli	Sequence 236, App	Sequence 742, App
SUMMAKIES			סו	US-09-867-159A-4	US-09-748-578-5	US-10-411-905-5	US-10-220-467A-2	US-10-436-782-24	US-09-880-748-2740	US-10-293-418-2740	US-09-851-138-204	US-09-988-493-162	US-10-007-363-4	US-10-807-553-4	US-10-820-467-236	US-10-699-114-742
			DB	10	σ	14	16	15	10	15	σ	10	13	16	17	11
			Match Length DB	10	10	10	ω	σ	80	æ	10	80	80	<b>a</b> 0	6	9
	æ	Query	Match	100.0	54.5	54.5	50.9	50.9	47.3	47.3	47.3	45.5	45.5	45.5	45.5	43.6
			Score	55	30	30	28	28	26	26	26	25	25	25	25	24
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Sequence 959, App Sequence 11, Appl	Sequence 705, App	164	210	164	210	164	210	22,	68	Seguence 167, App	213	57,	103,	56, Aj	Sequence 142, App	760,	1053,	105,	723,	289,	Sequence 176, App	Sequence 40, Appl	72,	Sequence 74, Appl	76,	84,	9	Sequence 106, App	21	Sequence 414, App
7 US-10-699-114-959 7 US-10-806-924-11	7 US-10-806-924-705	US-10	4 US-10-052-578-210	US-1	US-10	US-10	4 US-10-053-498B-210	5 US-10-258-146A-22	5 US-10-258-146A-68	5 US-10-328-953-167	5 US-10-328-953-213			US-09-826-177-56	5 US-10-428-335-142		7 US-10-699-114-1053	17 US-10-806-924-105	7 US-10-806-924-723	5 US-10-285-394-289	5 US-10-601-837-176	US-09-826-177-40	US-09-826-177-72	US-09-826-177-74	US-09-826-177-76	US-09-826-177-84	_	_	6 US-10-415-014-219	6 US-10-415-014-414
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14 24 15 24	16 24	17 24	18 24	19 24	20 24	21 24	22 24	23 24	24 24	25 24	26 24	27 24	28 24	29 24	30 24	31 23	32 23	33 , 23	34 23	35 23	36 23	37 23	38 23	39 23	40 23	41 23	42 23	43 23	44 23	45 23

## ALIGNMENTS

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APPLICANT: ANTIALIS
TITLE OF INVENTION: And at least one anti-histamine compound
TITLE OF INVENTION: And at least one anti-histamine compound
TITLE OF INVENTION: And at least one anti-histamine compound
FITLE OF INVENTION: And at least one anti-histamine compound
FILE REFERENCE: B112812US-antials
CURRENT APPLICATION NUMBER: US/09/867,159A
PRIOR APPLICATION NUMBER: FR01/04370
PRIOR APPLICATION NUMBER: FR01/04370
PRIOR APPLICATION NUMBER: FR01/05929
PRIOR APPLICATION NUMBER: FR01/05929
PRIOR APPLICATION NUMBER: FR01-05-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : LOCATION: (1)..(10)
; OTHER INFORMATION: Comprises epitope from cystine protease.
US-09-867-159A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Dermatophagoides pteronyssinus
FEATURE:
NAME/KEY: peptide
                   Sequence 4, Application US/09867159A Publication No. US20030104013A1 GENERAL INFORMATION:
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US-09-867-159A-4
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US-10-220-467A-2
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Publication No. US20030166012A1
GENERAL INFORMATION
APPLICANT: Blacin, Alan D.
APPLICANT: Blancon, Gary A.
TITLE OF INVENTION: Puffied (1,2-xylosyltransferase and Uses Thereof
FILE REFERENCE: D6063/D2
CURRENT APPLICATION NUMBER: US/10/411,905
CURRENT APPLICATION NUMBER: US/03-04-11
PRIOR FILING DATE: 2003-04-11
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 5.
LENGTH: 10
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      Sequence 5, Application US/09748578

Patent No. US20010016344A1

GENERAL INFORMATION:

APPLICANT: Blbein, Alan D.

APPLICANT: Bannon, Gary A.

TITLE OF INVENTION: Purified (1,2-Xylosyltransferase and Uses Thereof CURRENT APPLICATION NUMBER: US/09/748,578

CURRENT APPLICATION NUMBER: US/09/748,578

CURRENT FILING DATE: 2000-12-22

PRIOR FILING DATE: 1998-12-08

NUMBER OF SEQ ID NOS: 7

SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Amino acid sequence of a peptide released by Endo ; OTHER INFORMATION: 1ys C digestion of purified xylosyltransferase. US-09-748-578-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10220467A
Publication No. US20040121325A1
GENERAL INFORMATION:
APPLICANT: Glossl Prof., Josef
TITLE OF INVENTION: Beta 1, 2-Xylosyltransferase-gene from Arabidopis FILE REFERENCE: SONN:019US
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Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.5%; Score 30; DB 9; Length 10; 66.7%; Pred. No. 60;
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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4 YHAINL 9
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ORGANISM: soybean
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ORGANISM: soybean
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US-10-220-467A-2
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US-10-411-905-5
JS-09-748-578-5
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APPLICANT: Kinch, Michael
APPLICANT: Kinch, Michael
APPLICANT: Carles-Kinch, Kelly
APPLICANT: Carles-Kinch, Kelly
APPLICANT: Carles-Kinch, Kelly
APPLICANT: Carles-Kinch, Michael
APPLICANT: Langermann, Solomon
TITLE OF INVENTION: Epha2 Monoclonal Antibodies and Methods of Use Thereof
FILE REPERBRUCE: 10271-097
CURRENT APPLICATION NUMBER: US/10/436,782
CURRENT FILING DATE: 2003-05-12
PRIOR PILING DATE: 2002-05-10
PRIOR PLICATION NUMBER: 60/418,213
PRIOR FILING DATE: 2002-10-14
PRIOR FILING DATE: 2003-04-03
PRIOR FILING DATE: 2003-04-03
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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Squence 2740, Application US/09080748
Publication No. US20030059937A1
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR PLILING DATE: 2000-66-15
PRIOR PLILING DATE: 2000-615
PRIOR PLILING DATE: 2000-615
PRIOR PLILING DATE: 2000-615
PRIOR PLILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
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Pred. No. 1.3e+06;
1; Mismatches 0;
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Pred. No. 1.3e+06;
2; Mismatches 1;
CURRENT APPLICATION NUMBER: US/10/220,467A
CURRENT FILING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: A 355/2000
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/10436782; Publication No. US20040028685A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       50.9%;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-436-782-24
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2 PRYHAMD 8
                                                                                                                                                                                           TYPE: PRT
ORGANISM: soyabean
                                                                                                                                                                                                                                                                                                                                                                                         4 YHAVN 8
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Gaps
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COMPUTER: Microsoft Word 6.0 / ASCII text output
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,138
FILING DATE: 09-May-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,075
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: BP 94870166.9
FILING DATE: 21 Oct 1994
APPLICATION NUMBER: BP 95870076.7
FILING DATE: 28 Jun 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
APPLICANT: O'Hare, Michael John
APPLICANT: Page, Martin John
APPLICANT: Page, Martin John
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Waterfield, Michael Derek
TITLE OF INVENTION: Proteins, Genes, and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer
FILE REPERENCE: 25431-1-024
CURRENT APPLICATION NUMBER: US/09/988,493
CURRENT FILING DATE: 2002-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 47.3%; Score 26; DB 9; Length 10; Best Local Similarity 57.1%; Pred. No. 3.3e+02; Matches 4; Conservative 1; Mismatches 2; Indels
                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS:004
INFORMATION FOR SEQ ID NO: 204:
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PRIOR FILING DATE: 2001-03-20
PRIOR PILING DATE: 2001-03-20
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
PRIOR PILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 308
SEQ ID NO 162
SEQ ID NO 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 204:
US-09-851-138-204
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Publication No. US20030064419A1
GENERAL INFORMATION:
                                                                                                                                                                COUNTRY: USA
ZIR: 77210-4433
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 10 amino acids
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                    NUMBER OF SEQUENCES: 207
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US-09-988-493-162
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Publication No. US20020183508A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
STUTVER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Fublication No. US2003022396A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
FRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-16
PRIOR PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-01-17
PRIOR PRIOR PRILICATION NUMBER: 60/277,379
PRIOR PRILICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
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                                                                                                                                                                                                                                                                                                                 47.3%; Score 26; DB 10; Length 8; 37.5%; Pred. No. 1.3e+06;
                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
FRIOR APPLICATION NOTES PRIOR APPLICATION NUMBER: 60/293,499
FRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
IRNGTH: 8
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Best Local Similarity 37.9
Matches 3; Conservative
                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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PSYHYMDV 8
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PSYHYMDV 8
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                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 3, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-10-293-418-2740
                                                                                                                                                                                                                                                                US-09-880-748-2740
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                                                                                                                                                                                                                                                                                                                    Query Match
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Tue May 24 05:56:09 2005

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APPLICANT: Dana Ault-Riche
APPLICANT: Bruce Atkinson
APPLICANT: Bruce Atkinson
APPLICANT: Extendand Kumble
APPLICANT: Krishnanada Kumble
APPLICANT: Criste Sperinde
TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND METH(
TITLE OF INVENTION: USING THE SYSTEMS
FILE REFERENCE: 25885-1759
CURRENT PAPLICATION NUMBER: 05/423,018
PRIOR APPLICATION NUMBER: 60/423,018
PRIOR APPLICATION NUMBER: 60/422,923
PRIOR FILING DATE: 2002-10-30
PRIOR FILING DATE: 2002-10-30
PRIOR FILING DATE: 2002-10-30
PRIOR FILING DATE: 2002-10-30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 742
LENGTH: 6
                                                                                                                                                              US-10-820-467-236

i Sequence 226, Application US/10820467

i Sequence 226, Application US/10820467

i Sequence 226, Application No. US20050054053A1

i GENERAL INFORMATION:

APPLICANT: Beyna, Amelia Joy

APPLICANT: Beyna, Amelia Joy

APPLICANT: Cho, Ho, Sung

APPLICANT: Muchal, Umesh

APPLICANT: Willegas, Michael Francis Aquino

APPLICANT: Villegas, Michael Francis Aquino

APPLICANT: Villegas, Michael Bephen

TITLE OF INVENTION: INTERFERON VARIANTS WITH IMIPROVED PROPERTIES

TITLE OF INVENTION: INTERFERON VARIANTS WITH IMIPROVED PROPERTIES

TITLE OF INVENTION: UNBER: US/10/820,467

CURRENT APPLICATION NUMBER: US 60/477,246

PRIOR FILING DATE: 2003-06-10

PRIOR APPLICATION NUMBER: US 60/489,725

PRIOR APPLICATION NUMBER: US 60/489,725

PRIOR PILING DATE: 2003-06-10

PRIOR PILING DATE: 2003-06-10

PRIOR PILING DATE: 2003-06-10

PRIOR PILING DATE: 2003-06-10

PRIOR PILING DATE: 2003-07-10-01

PRIOR PILING DATE: 2003-06-10

PRIOR PILING DATE: 2003-06-10

PRIOR PILING DATE: 2003-06-10

PRIOR PILING DATE: 2003-07-10-01

PRIOR PILING DATE: 2003-07-10-01

PRIOR PILING DATE: 2003-06-10

PRIOR PILING DATE: 2003-07-10-01

PRIOR PILING DATE: 2003-07-10-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 17; Length 9;
Pred. No. 1.3e+06;
1; Mismatches 1; Indels
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Publication No. US20050042623A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.73
Matches 4; Conservative
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ORGANISM: Artificial
PNYHAVNI
                                                                 1 PDYHDAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10007363;
Publication No. US20020168354A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENITON: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENITON: sechemia
TITLE OF INVENITON: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENITON: sechemia
TITLE OF INVENITOR: sechemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10807553;
Publication No. US20040186055A1;
Publication No. US20040186055A1;
Publication No. US20040186055A1;
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION:
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION NUMBER: US/10/800
CURRENT APPLICATION NUMBER: US/10/000,363
PRIOR APPLICATION NUMBER: US 60/247,830
PRIOR FILING DATE: 2000-11-10
PRIOR FILING DATE: 2000-11-10
PRIOR FILING DATE: 2000-11-10
SEQ ID NOS: 18
SEQ ID NOS: 18
LENGTH: BattSEQ for Windows Version 4.0
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; OTHER INFORMATION: scrambled pseudo-epsilon RACK octapeptide US-10-807-553-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: scrambled pseudo-epsilon RACK octapeptide US-10-007-363-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 45.5%; Score 25; DB 16; Length 8; Best Local Similarity 50.0%; Pred. No. 1.3e+06; Matches 4; Conservative 1; Mismatches 3; Indels
                              45.5%; Score 25; DB 10; Length 8; 80.0%; Pred. No. 1.3e+06;
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                                                                                                        1; Mismatches
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ORGANISM: Artificial Sequence
                       Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PNYHAVNI 9
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1 PDYHDAGI 8
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2 NFHAV 6
                                                                                                                                                                             3 NYHAV 7
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US-10-007-363-4
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Gaps

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Score 24; DB 17; Length 6; Pred. No. 1.3e+06; 1; Mismatches 1; Indels
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                                             43.6%;
                                           Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                           1 QPNYH S
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1 EPGYH 5
      US-10-806-924-11
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APPLICANT: Lynne Jersaitis
APPLICANT: Lynne Jersaitis
APPLICANT: Gizette Sperinde
APPLICANT: Gizette Sperinde
TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND METH
TITLE OF INVENTION: USING THE SYSTEMS
FILE REFERENCE: 25885-1759
CURRENT APPLICATION NUMBER: (05/102,018
PRIOR PILING DATE: 2002-10-30
PRIOR PILING DATE: 2002-10-30
PRIOR PILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 1094
SEQ ID NO 959
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-10-806-924-11
Sequence 11, Application US/10806924
Sequence 11, Application No. US20050095648A1
Sequence 11, Application No. US20050095648A1
September 11, Moremation:
The Comparity of the Mario Septement of the Mario September 11 Authority of the Morematican Sequence 11 Tile OF INVENTION: and polypeptide epitopes
TITLE OF INVENTION: and polypeptide epitopes
FILE REFERENCE: 25885-1760
CURRENT APPLICATION NUMBER: US/10/806,924
CURRENT FILING DATE: 2004-03-22
NUMBER OF SEQ ID NOS: 911
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                           Score 24; DB 17; Length 6; Pred. No. 1.3e+06;
                                                                                                                                                                    1; Indels
                                                                                                                                                                        1; Mismatches
                                      FEATURE:
COTHER INFORMATION: synthetic peptide
US-10-699-114-742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: synthetic peptide US-10-699-114-959
                                                                                                                                                                                                                                                                                                                                                      Sequence 959, Application US/10699114
Publication No. US20050042623A1
GENERAL INFORMATION:
APPLICANT: Dana Ault-Riche
APPLICANT: Bruce Atkinson
APPLICANT: Krishnanand Kumble
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                           43.6%;
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ORGANISM: Artificial Sequence
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                                                                                                                                              Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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EPGYH 6
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1 EPGYH 5
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US-10-699-114-959
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LENGTH: 6
                                                                                                                               Query Match
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TYPE: PRT
ORGANISM: soybean
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Sequence 204, Appli
Sequence 204, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 181, Appl
Sequence 181, Appl
Sequence 181, Appl
Sequence 18, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 3, Appli
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                                                                                                                                   May 19, 2005, 17:53:34 ; Search time 29.5 Seconds (without alignments) 25.305 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-207-223-5
US-09-748-578-5
US-08-813-075-204
US-08-615-181-108
US-08-212-433A-33
US-08-212-433A-33
US-08-716-256-33
PCT-USS5-03239-33
5436320-3
5436320-3
5436320-3
5436320-3
US-08-877-605-181
US-08-877-605-181
US-08-877-605-181
US-08-877-605-181
US-08-877-605-181
US-08-977-605-181
US-08-977-605-181
US-08-977-605-220
US-08-98-110A-3
US-08-913-10A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                 513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                         US-09-867-159A-4
55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0 Maximum DB seq length: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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No.
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Sequence 12, Appl Sequence 14, Appl Sequence 3, Appl Sequence 3, Appl Sequence 16, Appl Sequence 16, Appl Sequence 104, Appl Sequence 44, Appl Sequence 28, Appl Sequence 28, Appl Sequence 19, Appl Sequence 19, Appl Sequence 34, Appl Sequence 60, Appl Sequence 60, Appl	and Uses Thereof	ide released by Endo lys C transferase.  Length 10;  ; Indels 0; Gaps 0;		and Uses Thereof
5 2 US-08-558-823-12 5 3 US-08-604-991-14 5 3 US-09-363-639-14 6 2 US-08-428-131-3 6 2 US-08-558-823-15 6 2 US-08-558-823-16 6 2 US-08-510-915-104 6 3 US-08-810-9104 6 3 US-08-811-089-104 6 3 US-08-811-089-104 6 3 US-08-915-395-19 6 3 US-09-115-395-19 6 3 US-09-301-085-104 6 3 US-09-301-085-104 6 3 US-09-301-085-104 6 3 US-09-501-102-44 6 3 US-09-501-102-44	ALIGNMENTS tion US/09207223 Alan D. Gary A. Gary A. NUMBER: US/09/207,223 E. 1998-12-08 E: 1997-12-08 E: 1997-12-08 SS: 7	Amino acid sequence of a peptide released digestion of purified xylosyltransferase.  54.5%; Score 30; DB 3; Length 10;  y 66.7%; Pred. No. 15;  rvative 2; Mismatches 0; Indels	·	US/09748578 n D. ry A. rified (1,2-Xylosyltransferase MBER: US/09/748,578 2000-12-22 ER: US 09/207,223 8-12-08
28 21 38.2 30 21 38.2 31 21 38.2 32 21 38.2 34 21 38.2 35 21 38.2 36 21 38.2 37 21 38.2 38 21 38.2 40 21 38.2 41 21 38.2 44 21 38.2 44 21 38.2 44 21 38.2	RESULT 1 US-09-207-223-5 Sequence 5, Application US/( Patent No. 6168937 GENERAL INFORMATION: APPLICANT: BLDein, Alan D. APPLICANT: Bannon, Gary A. TITLE OF INVENTION: FILE REFERENCE: D6063 CURRENT APPLICATION NUMBER CURRENT APPLICATION NUMBER CURRENT FILING DATE: 1998-18ALIER FILING DATE: 1998-18ALIER FILING DATE: 1998-18D IN OS: 7 SEQ ID NO 5 LENGTH: 10 TYPE: PRT CORGANISM: ROADBAN CORGAN	ORMATION: -5 Similarity 4; Conser	Oy 4 YHAVNI 9    : :  Db 4 YHAINL 9	RESULT 2 (Sequence 5, Application US/09748578 Fatent No. 6593462 GENERAL INFORMATION: APPLICANT: Blbein, Alan D. TITLE OF INVENTION: FILE REPERENCE: D6063/D0 FILE REPERENCE: D6063/D0 FILE REPERENCE: D6063/D0 FILE REPERENCE: D8063/D0 FILE REPERENC

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45.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-212-433A-33
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                                                                                                                                                                                                                                                                                   Sequence 204, Application US/08836075A
Patent No. 6180768
CENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: STUYVER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
TITLE OF INVENTION: AGENTS
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
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                                                                                                                    Gaps
CTHER INFORMATION: Amino acid sequence of a peptide released by Endo ; OTHER INFORMATION: 1ys C digestion of purified xylosyltransferase. US-09-748-578-5
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                                                                             Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,075A
FILING DATE: 21 Apr 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/04155
FILING DATE: 23 Oct 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94870166.9
FILING DATE: 21 Oct 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 Jun 1995
ATTORNEY/AGENT INFORMATION:
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,778
REGISTRATION NUMBER: 29,778
REGISTRATION NUMBER: 29,778
                                                                           Score 30; DB 4;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                   2; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ARNOLD, WHITE & DURKEE STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INNS:004
                                                                           54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 5/...
4, Conservative
                                                                       Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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YHAINL 9
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US-08-836-075A-204
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US-08-615-181-108
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Sequence 108, Application US/08615181

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GENERAL INTOWANTION:

APPLICANT: WINA, KINGRIL
APPLICANT: WINA ALXINGRIL
APPLICANT: WINA ALXINGRIL
ADDRESSES: P.C.
COMESSES: P.C.
STREET: 122026

COMPRISED: P.C. SPIVAK, MCCLELLAND, MAIRE & NEUSTADT,
ADDRESSES: P.C.
STREET: 122026

COMPRISED: P.C. SPIVAK, MCCLELLAND, MAIRE & NEUSTADT,
ADDRESSES: P.C.
COMPRISED: P.C. SPIVAK, MCCLELLAND, MAIRE & NEUSTADT,
ADDRESSES: P.C.
COMPRISED: P.C. SPIVAK, MCCLELLAND, MAIRE & NEUSTADT,
ADDRESSES: P.C.
COMPRISED: P.C. SPIVAK, MCCLELLAND, MAIRE & NEUSTADT,
ADDRESSES: P.C.
COMPRISED: P.C. SPIVAK, MCCLELLAND, MAIRE & NEUSTADT,
ADDRESSES: P.C. SPIVAK, MCCLELLAND, MAIRE & NEUSTADT,
ADDRESSES: P.C.
COMPRISED: P.C. SPIVAK, MCCLELLAND, MAIRE & NEUSTADT,
ADDRESSES: P.C. SPIVAK, MCCLELLAND, MAIRE & NEUSTADT,
ADDRESSES, P.C. SPIVAK, MCCLELLAND, MAIRE & NEUSTADT,
ADDRESSES, P.C. SPIVAK, MCCLELLAND, MCCLELL
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Query Match
Best Local Similarity 100...
A; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 amino acids
                                                                                                                                                                                                                               4; Conservative
                           TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-716-256-33
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STRANDEDNESS: single
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                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
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STRANDEDNESS:
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Patent No. 5436320
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PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
CARBONHATE SEQUENCES IN DATABASES OR TO IDENTIFY
ORGANISMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,433A
FILING DATE: 14-MAR-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: HUGHAS, Richard L.
REGISTRATION NUMBER: 31,264
REFERENCE/DOCKET NUMBER: 16336-2
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
TELEPHONE: 415-543-5043
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,256
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PILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03239
FILING DATE: 14-MAR-1995
APPLICATION NUMBER: US 08/212,433
FILING DATE: 14-MAR-1994
ATTORNEY AGENT INFORMATION:
NAME: PARMELE, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 16336-2PC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: USE OF MASS SPECTIONS OF INVENTION: USE OF MASS SPECTITLE OF INVENTION: CARBOHYDRATE SECTITLE OF INVENTION: CARBOHYDRATE SECTITLE OF INVENTION: ORGANISMS NUMBER OF SEQUENCES: 46
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-08-716-256-33
Sequence 33, Application US/08716256
Patent No. 6017693
GENERAL INFORMATION:
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100.0%; Pre
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                       94105-1492
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Query Match
     Matches
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CURRENT FILING DATE: 1997-06-18
NUMBER OF SEQ ID NOS: 353
SEGTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 181
LENGTH: 6
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5436320-3

FRECHT NO. 5436320

FRECHT NO. 5436320

APPLICANT: SPIEGEL, ALLEN M.

TITLE OF INVENTION: ANTIBODY REAGENTS THAT IDENTIFY THE

CARBOXY-TERMINAL PEPTIDE OF THE GTP-BINDING PROTEIN G

NUMBER OF SEQUENCES: 10

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 18-70A-1992

FILING DATE: 14-7AN-1992

FILING DATE: 08-AUG-1990

FILING DATE: 10-70A-1999

FILING DATE: 15-JUN-1989

APPLICATION NUMBER: 365,919

FILING DATE: 25-SEP-1987
                                                                                                                                                      Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.5%; Score 25; DB 6; Length 10; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                        DB 6; Len.
                                                                                                                                                                                       Mismatches
                                                                                                                                                      Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Peptide X Library US-08-877-605-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 181, Application US/08877605
Patent No. 6582965
                                                                                                                                                                     ilarity 100.0%; P
Conservative 0;
FILING DATE: 08-AUG-1990
APPLICATION NUMBER: 365,919
FILING DATE: 15-JUN-1989
APPLICATION NUMBER: 10,909
FILING DATE: 25-SEP-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                      45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Robert Townsend
APPLICANT: Raj Parekh
APPLICANT: Sally Prime
APPLICANT: NICK Webb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 OPNY 9
                                                                                                                                                                                                                                                        OPNY 9
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                                                                                                     LENGTH: 10
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US-08-877-605-181
                                                                                   SEQ ID NO:3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5436320-3
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Length 6;

41.8%; Score 23; DB 4; 1 60.0%; Pred. No. 4.1e+05;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                   ON: A METHOD FOR DE NOVO PEPTIDE SEQUENCE DETERMINATION 9195-004
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MEDIUM TYPE: Floppy disk

COMPUTER: IN PC compatible

COMPUTER: IN PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOSTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/057,363C

FILING DATE: 08-Apr-1998

CLASSIFICATION: -(Unknown)

ATTORNEY AGENT INFORMATION:

NAME: Christiansen, William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 100086.406

TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:
ADDRESSEE. Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6;
 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.8%; Score 23; DB 4; I 60.0%; Pred. No. 4.1e+05; trive 2; Mismatches 0
Mismatches
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/877,605
CURRENT FILING DATE: 1997-06-18
NUMBER OF SEQ ID NOS: 353
SEQ ID NO 220
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Peptide X Library US-08-877-605-220
                                                                                                                                                      Sequence 220, Application US/08877605
Patent No. 6582965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Robert Townsend
APPLICANT: Raj Parckh
APPLICANT: Sally Prime
APPLICANT: Sally Prime
TITLE OF INVENTION: A METHOD
FILE REFERENCE: 9195-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 60.0
Matches 3; Conservative
3; Conservative
                                   4 YHAVN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 NYHAV 7
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1 DYHAI 5
                                                                    1 YHAID 5
                                                                                                                                          US-08-877-605-220
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CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.075
TELECOMMUNICATION INFORMATION:
TELEFAX: (404) 688-0980
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEPHONE: (404) 688-9880
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/273,474
FILING DATE: 13-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                             40.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.0%;
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Best Local Similarity 66.7;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                         LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 amino acids
                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-092-110A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                          3 NYHAVN 8
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
ATTLE OP INVENTION: COMPOUNDS AND METHODS FOR STIMULATING
TITLE OP INVENTION: GENE EXPRESSION AND CELLULAR DIFFERENTIATION
FILE REFERENCE: 100086.406C1
CURRENT APPLICATION NUMBER: US/09/265,107A
CURRENT FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Patent No. 558477
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kilpatrick, David R.
TITLE OF INVENTION: METHODS OF DETECTION UTILIZING THE SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, The Candler Building, 127
STREET: Peachtree Street, NE
                                                                                                                                                           40.0%; Score 22; DB 4; Length 4; 100.0%; Pred. No. 4.1e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.0%; Score 22; DB 4; Length 4; 100.0%; Pred. No. 4.1e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/092,110A
FILING DATE: 13-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Linear peptide modulating agent
US-09-265-107-18
                                                                  TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 18: US-09-057-363C-18
                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 18, Application US/09265107A; Patent No. 6683048
                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Thea 4; Conservative
                                                                                                                                               Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                            5 HAVN 8
                                                                                                                                                                                                                                                                     1 HAVN 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAVN 8
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US-09-265-107-18
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US-08-092-110A-3
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0
                                                                                                                                                                                                                                                 Sequence 3, Application US/08273474

Patent No. 5691134

GENERAL INFORMATION:
APPLICANT: KIJPALTICK, David R.
TITLE OF INVENTION: POLIOVIRUS SPECIFIC PRIMERS AND METHODS
TITLE OF INVENTION: 0F DETECTION UTLLIZING THE SAME
NUMBER OF SEQUENCES 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, The Candler Building, 127
STREET: Peachtree Street, NE
Score 22; DB 1; Length 7; Pred. No. 4.1e+05; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 1; Length 7; Pred. No. 4.1e+05; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30103-1811
COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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| ||:| 2 NGHALN 7

Search completed: May 19, 2005, 18:11:53 Job time : 30.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 19, 2005, 18:16:02 ; Search time 38 Seconds (without alignments) 22.788 Million cell updates/sec Run on:

US-09-867-159A-5 57

1 WTVRNSWDT 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

791 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	26	45.6	6	~	PT0299	Ig heavy chain CRD
7	22	38.6	S	~	PT0580	T-cell receptor be
m	22	38.6	80	~	A38887	T-cell receptor ga
4	19	33.3	6	7	A24244	adipokinetic hormo
ß	18	31.6	9	~	A31263	dihydrofolate redu
9	17	29.8	9	7	PT0519	T-cell receptor be
7	17	29.8	7	7	S33244	
80	17	29.8	7	7	S33245	neuromodulatory pe
σ	17	29.8	7	N	S33246	dulatory
10	16	28.1	4	7	PT0661	tor
11	16	28.1	9	7	A61068	locustakinin - mig
12	16	28.1	7	~	PH1602	÷
13	16	28.1	7	4	155382	hypothetical pepti
	16	28.1	80	N	S19288	
15	16	28.1	80	7	JS0315	leucokinin V - Mad
16	16	28.1	60	7	JS0316	leucokinin VI - Ma
17	16	28.1	œ	7	JS0317	leucokinin VII - M
18	16	28.1	9	7	A43848	cell surface adhes
13	15	9	9	7	B31263	
20	15	26.3	7	7	PN0649	
21	15	26.3	7	7	A61081	tryptophyllin, bas
22	15	26.3	80	7	S10596	adipokinetic hormo
23	15	26.3	80	N	JS0318	leucokinin VIII -
24	15	26.3	σ,	~	S07205	litorin 2-Glu - Au
25	15	9	9	~	S07204	litorin I - Austra
26	15	9	σ	7	PT0231	Ig heavy chain CDR
27	15	26.3	σ	7	I58350	gene c-mpl protein
	15	26.3	σ	7	PC2021	oxytocin-related p
29	15	26.3	Φ	7	D57444	neuropeptide Grb-A

2 PT0308 2 S66195 2 A28495 2 B28495 2 S07241 2 S07240 2 PT0690 2 PT0630 2 PT0630 2 PT0630 2 S09066 2 S09066 2 B44960 2 S09996 2 A59495	Ig heavy chain CRD	alcohol dehydrogen	conopressin G - co	conopressin S - co	litorin - Rohde's	Ig heavy chain CRD	lysine-conopressin	T-cell receptor be	cerebellar degener	T-cell receptor be	pev-kinin 2 - pena	globulin IV alpha	neuropeptide Led-C	hypertrehalosemic	adipokinetic hormo	Vesicle associated
0000000000000000	PT0308	866195	A28495	B28495	S07241	PT0270	S39040	PT0690	B35640	PT0630	PD0028	990608	B44960	966808	B49823	A59495
	7	7	7	7	7	7	7	7	~	8	7	7	0	~	7	7
	24.6	24.6	24.6	24.6	24.6	24.6	24.6	22.8	22.8	22.8	22:8	22.8	22.8	22.8	22.8	22.8
4 4 4 4 4 4 4 4 4 2 2 2 2 2 2 2 2 2 2 2	14	14	14	14	14	14	14	13	13	13	13	13	13	13	13	13
14 24.6 14 24.6 14 24.6 14 24.6 14 24.6 14 24.6 13 22.8 13 22.8 13 22.8 13 22.8 13 22.8 13 22.8 13 22.8 13 22.8 13 22.8 13 22.8	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

Ig heavy chain CRD3 region (clone 5-103B) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0299
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Molecule type: DNA A;Residues: 1-9 <YAM> A;Experimental Bource: B lymphocyte C;Keywords: heterotetramer; immunoglobulin

ö Gaps ö 45.6%; Score 26; DB 2; Length 9; 80.0%; Pred. No. 2.8e+05; ative 0; Mismatches 1; Indels 4; Conservative Query Match Best Local Similarity Matches

4 RNSWD 8 1 RESWD 5 셤 ઠે

T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997 C;Accession: PT0580

R;Feeney, A.J. J. Exp. Med. 114, 115-124, 1991 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558

A,Accession: PT0580
A,Status: translation not shown
A,Status: translation not shown
A,Molecule type: mRNA
A,Residues: 1-5 <FEEA
A,Experimental source: day 19 fetal thymus, strain BALB/C
C,Keywords: T-cell receptor

.; 0 Query Match 38.6%; Score 22; DB 2; Length 5; Best Local Similarity 75.0%; Pred. No. 2.8e+05; Matches 3; Conservative 1; Mismatches 0; Indels

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Gaps

:||| 2 SSWD 5 g

5 NSWD 8

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RESULT 3

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Riminkata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FRBS Lett. 323, 104-108, 1993
A;Title: Wammide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the A;Reference number: S33244; MUID:93265912; PMID:8495720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Accession: S33245
R,Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A,Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the A,Reference number: S33244; MUID:93265912; PMID:8495720
                                                                                                                                                                                                                                                                                                                      R.Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
J. Exp. Med. 174, 115-124, 1991
A.Titler Juncitional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0519
                                                                                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuromodulatory peptide WMamide-1 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar.1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S33244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuromodulatory peptide WWamide-2 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar.1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Aceession: S33245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                        receptor beta chain V-D-J region (100-4C) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.8%; Score 17; DB 2; Length 6; 100.0%; Pred. No. 2.8e+05; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.8%; Score 17; DB 2; Length 7;
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Pred. No. 2.8e+05;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Molecule type: mRNA
A Residues: 1-6 <PES>
A Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPROT: P35921
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Best Local Similarity 28.6
Matches 2, Conservative
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A, Status: preliminary
A, Molecule type: protein
A, Residues: 1-7 < MIN>
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A; Status: preliminary
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CiSpecies: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
CiSpecies: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
CiDate: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
CiAccession: A2444
RiJaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway Biochem. Biophys. Res. Commun. 135, 622-628, 1986
A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helic A;Reference number: A2424; MUID:86186794; PMID:3964263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: UNIPROT:P08901
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9/Modified site: amidated carboxyl end (Gly) #status experimental
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R;Peterson, D.S.; Walliker, D.; Wellems, T.E.
Proc. Natl. Acad. Sci. U.S.A. 65, 9114-9118, 1988
A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A;Reference number: A94217; MUID:89057886; PMID:2904149
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dihydrofolate reductase (BC 1.5.1.3) / thymidylate synthase (BC 2.1.1.45) - Plasmodium
C;Species: Plasmodium falciparum
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
                                                   C;Species: Mus musculus (house mouse) (inguienc)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: A38887
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma shaccession: A38887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 31.6%; Score 18; DB 2; Length 6; Best Local Similarity 50.0%; Pred. No. 2.8e+05; Matches 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                38.6%; Score 22; DB 2; Length 8; 75.0%; Pred. No. 2.8e+05;
A38887
T-cell receptor gamma chain (5t.2) - mouse (fragment)
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A24244
adipokinetic hormone - bollworm
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A;Molecule type: protein
A;Residues: 1-9 <JAF>
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SWDS 5
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PH1602

19 H chain V-D-J region (wild-type clone 313) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Paccession: PH1602

B;Levinson, D.A.; Campos Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993

J; Exp. Med. 178, 317-329, 1993

J; Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A;Accession: PH1602
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R;Dawson, S.J; Wiman, B.; Hamsten, A.; Green, F.; Humphries, S.; Henney, A.M.
J; Biol. Chem. 268, 10739-10745, 1993
A;Title: The two allele sequences of a common polymorphism in the promoter of the plasmi A;Reference number: I55382; MUID:93266509; PMID:8388372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: GB:M91557, NID:g190020, PIDN:AAA60110.1, PID:g190021
C,Comment: This is the hypothetical translation of a sequence from the PAI1 gene promote
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C;Species: Homo sapiens (man)
C;Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 20-Apr-2000
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C;Species: Kluyvera cryocrescens
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                  Gaps
A;Cross-references: UNIPROT:P41491
C;Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide
F;6/Modified site: amidated carboxyl end (Gly) #status experimental
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                                                                                                                                                28.1%; Score 16; DB 2; Length 6; 66.7%; Pred. No. 2.8e+05; ative 1; Mismatches 0; Indels
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A;Molecule type: DNA
A;Residues: 1-7 <DAW>
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Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0;
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A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin
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A, Map position: 7q21.3-7q22
                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 2; Conservative
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S19288
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C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession. A61068
R;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.
Regul. Pept. 37, 49-57, 1992
A;Title: Locustafinin, a novel myotropic peptide from Locusta migratoria, isolation, pri
A;Reference number: A61068; MUID:92262851; PMID:1585017
                                                                                                                                                                                                                                                                                                                                                                      neuromodulatory peptide Wwamide-3 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: 533246
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
A;Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of A;Reference number: 53244, MUID:93265912; PMID:8495720
A;Accession: 533246
A;Accession: S3246
A;Accession: 
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A,Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A,Reference number: PT0509; MUID:91277601; PMID:1711558
A,Accession: PT0661
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PT0661
T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: PT0661
R;Feeney, A.J.
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A;Experimental source: day 4 postnatal thymus, strain BALB/c
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.8%; Score 17; DB 2; 1
28.6%; Pred. No. 2.8e+05;
tive 1; Mismatches 4.
28.6%; Pred. No. 2.8e+05; ive 1; Mismatches 4
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Best Local Similarity 28.6
Matches 2; Conservative
Best Local Similarity 28.6
Matches 2; Conservative
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C;Accession: S19288
R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
Bacchem. J. 280, 659-662, 1991
A;Tile: Chemical modification of serine at the active site of penicillin acylase from FA;Reference number: S19288, MUID:92109664; PMID:1764029
A;Accession: S19288
A;Accession: S19288
A;Statuse preliminary
A;Molecule type: protein
A;Residues: 1.8 <MAR>
A;Cross-references: UNIPROT:Q7M124
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C;Species: Leucophaea maderae (Madeira cockroach)
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0315
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic A;Reference number: JS0315
A;Accession: JS0315
A;Accession: JS0315
A;Accession: JS0315
A;Accession: JS0315
A;Accession: JS0315
A;Cosse-references: UNFROT:P19987
C;Cossent: Leucokinins, a family of cephalomyotropic peptide
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

leucokinin V - Madeira cockroach

Gaps ö Query Match 28.1%; Score 16; DB 2; Length 8; Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 0; Indels

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:|| 5 SSW 7 5 NSW 7

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Search completed: May 19, 2005, 18:26:29 Job time : 40 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 19, 2005, 18:12:01; Search time 173 Seconds (without alignments) 26.640 Million cell updates/sec

US-09-867-159A-5 57 1 WTVRNSWDT 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1455 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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||: ||| WTL---WDT 1 WTVRNSWDT

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		Description	238366 bacteriopha	Q9h3y3 homo sapien	-	Q8g104 borrelia bu							_	Q9r9c4 borrelia bu				Q8gl31 borrelia bu	P83661 cyphononyx		P35920 achatina fu		049223 glycine max			Q61db5 homo sapien	Q673w5 tyrannus me		Q673w7 telophorus				2673x1 rhipidura a
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SUMMAKIES		QI	Q38366	Q9H3Y3	OCP3_OCTMI	Q8GL04	LCK1_LEUMA		PK1 PERAM	PK3_PERAM	PK5_PERAM	Q8G940	Q8GL26	Q9R9C4	037854	Q8GL21	AKH_HELZE	Q8G <u>L</u> 31	C125_CYPDO		WWA2_ACHFU	WWA3 ACHFU	049223	Q62721	P79940	QGLDBS	Q673W5	Q673W6	Q673W7	Q673W8	Q673W9	Q673X0	Q673X1
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		Score	7	25	21	21	21	21	21	21	21	21	21	21	19	19	19	19	18	17	17	17	17	17	17	17	17	17	17	17	17	17	17
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
01-DBS-2011 (Novel protein with a Kunitz/Bovine pancreatic trypsin inhibitor domain and WaP-type (Whey Acidic Protein) 'four-disulfide core' domains) (Fragment).

9 AA.

PRT;

PRELIMINARY;

09нзуз

RESULT 2 09H3Y3

Name=dJ461P17.1;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Lloyd D.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; All21778; CAB76844.1; -.
NON TER 9 9 SEQÜENCE 9 AA; 1036 MW; 2C417B01B412D1B3 CRC64;

SEQUENCE FROM N.A.

0673x2 pseudobias 0673x4 prionops sc 0673x5 placysteira 0673x5 oriolus xan 0673x6 oriolus xan 0673x8 bias flammu 0673x9 malaconotus 0673y1 lanioturdus 0673y1 lanioturdus 0673y2 laniarius 1 0673y3 laniarius 1 0673y3 laniarius 6	·		regulation of	Length 9; Indels 3; Gaps 1;
9 2 0673X2 9 2 0673X3 9 2 0673X4 9 2 0673X4 9 2 0673X6 9 2 0673X7 9 2 0673X9 9 2 0673Y1 9 2 0673Y1 9 2 0673Y2 9 2 0673Y3 9 2 0673Y3	ALIGNMENTS RY; PRT; 9 AA.	1. 01, Created) 1. 01, Last sequence update) 1. 19, Last annotation update) ent). 4. 8; Microviridae, Microvirus.	termination in the gene.";	2%; Score 27.5; DB 2; L 6%; Pred. No. 1.6e+06; 1; Mismatches 0;
32 17 29.8 34 17 29.8 35 17 29.8 36 17 29.8 36 17 29.8 38 17 29.8 40 17 29.8 41 17 29.8 42 17 29.8 44 17 29.8 44 17 29.8	RESULT 1 Q38366 D Q38366. PRELIMINARY		SEQUENCE FROM MEDLINE=881189 Buckley K.J., ROL of prema expression of J. Mol. Biol. EMBL, X07809; NON TER	Query Match Best Local Similarity 55. Matches 5; Conservative

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Stevenson B., Miller J.C.;
"Intra- and interbacterial genetic exchange of Lyme disease spirochete erp genes generates sequence identity amidst diversity.";
J. Mol. Evol. 57:309-324(2003).
EMBL; AY142103; AAN17648.1; -.
                                                                                                                                                                                                                                                                               36.8%; Score 21; DB 2; Length 7; 40.0%; Pred. No. 1.6e+06; vative 2; Mismatches 1; Indels
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Matches 2; Conservative
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P21140;
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P21142;
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SEQUENCE
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LCK3 LEUMA
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LCK1 LEUMA
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-!- FUNCTION: Cardioactive; has both positive chronotropic and inotropic effects on the heart. Ocp-4 is a 1000 time less active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  than Ocp.3.

-!- SUBCELDULAR LOCATION: Secreted.
-!- PTM: Ocp.4 has D-Ser instead of L-Ser.
-!- MASS SPECTROMETRY: WW=395.2; METHOD=MADI; RANGE=1-4; NOTE=Ref.1.
D-amino acid; Direct protein sequencing; Hormone.
MOD RES 2 2 D-serine (in form Ocp.4).
RSD 2 2 CHAPPER (in form Ocp.4).
RSD 2 2 CHAPPER (in form Ocp.4).
RSD 2 2 CHAPPER (in form Ocp.4).
                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid group cp32-5.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia
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MEDIINE=22610300; PubMed=12724373; DOI=10.1099/mic.0.26120-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.8%; Score 21; DB 1; Length 4; 100.0%; Pred. No. 1.6e+06; tive 0; Mismatches 0; Indels
h similarity 100.0%; Score 25; DB 2; Length 9; Similarity 100.0%; Pred. No. 1.6e+06; 4; Conservative 0; Mismatches 0; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Cardioactive peptides Ocp-3/Ocp-4.
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MEDLINE=22990544; PubMed=14629041;
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Microbiology 149:1113-1125(2003)
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28-FEB-2003 (Rel. 41, Last seq
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Name=PF-50;
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      Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                   1 WTVR 4
                                                                                                                                                                                            WTVR 5
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                                                                                                                                                                                                                                                                                      RESULT 3

10 79-0073

10 70-0073

10 728-FEB

10 728-FEB

10 728-FEB

10 8-5-VIL

11 8-5-VIL

11 8-5-VIL

12 8-5-VIL

13 8-5-VIL

14 8-5-VIL

15 8-5-VIL

16 8-5-VIL

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18 8-5-VIL

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19 8-5-VIL

10 8-5-V
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Q8GL04
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"Isolation, primary structure and synthesis of two neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotropins.";
Comp. Biochem. Physiol. 84C:205-211(1986).
-!- FONGTION: This cephalomyotropic peptide stimulates contractile activity of cockroach protodeum (hindgut).
-!- SUBCELLULAR LOCATION: Secreted.
Amidation; Direct protoin sequencing; Neuropeptide.
MOD RES

8 8 Glycine amide.

Glycine amide.

SEQÜENCE 8 AA; 893 MW; DC6365B449CDC76A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Head; Holman G.M., Cook B.J., Nachman R.J.; Althous G.M., Cook B.J., Nachman R.J.; Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotropins.";
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                                                                                            01-MAY-1991 (Rel. 18, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Leucokinin I (L.I.)
Leucophae maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blabtraria; Blaberoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Orthopteroidea, Dictyoptera, Blattaria, Blaberoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 8;
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Pred. No. 1.6e+06;
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01-MAY-1991 (Rel. 18, Last sequence update)
05-UIL-2004 (Rel. 44, Last annotation update)
Leucokinin III (L-III).
8 AA.
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                                                                 01-MAY-1991 (Rel. 18, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                   Blaberidae, Leucophaea.
NCBI_TaxID=6988;
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NCBI_TaxID=6988;
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NCBI_TaxID=6978;
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                                                                                                            americana.";
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P82689;
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-!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Corpora cardiaca;
MEDLINE=981010462; PubMed=9350979; DOI=10.1016/S0167-0115(97)01029-X;
Predel R., Kellner R., Rapus J., Penzlin H., Gade G.;
"Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Comp. Biochem. Physiol. 84C:271-276 (1986).
-!-FUNCTION: This cephalomyotropic peptide stimulates contractile activity of cockroach procdeum (hindgut).
-!- SUBCELLULAR LOCATION: Secreted.
--- Amidation; Direct protein sequencing, Neuropeptide.
MOD RES
SEQUENCE 8 AA, 910 MW, DC6365B449C866DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MASS SPECTROMETRY: MW=949.26; METHOD=Electrospray; RANGE=1-8;
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05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Kinin-3 (Pea-K-3).
Periplaneta americana (American cockroach).
Bukaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Periplaneta americana (American cockroach).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Orthopteroidea, Dictyoptera, Blattaria, Blattoidea,
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                                                                                                                                                                      Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE=Ref.1.
-!- SIMILARITY: Belongs to the kinin family.
Amidation; Direct procein sequencing; Neuropeptide.
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8 AA; 950 MW; 326365B449D5A774 CRC64;
                                                                                                                                                                    Score 21; DB 1; L
Pred. No. 1.6e+06;
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(Rel. 44, Last sequence update)
(Rel. 44, Last annotation update)
                                                                                                                                                     36.8%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
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                                                                                                                                                                                                                  Conservative
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NCBI_TaxID=6978;
                                                                                                                                                                      Query Match
Best Local Similarity
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05-JUL-2004
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PUPERAM
ID PAC P8268
PAC P8268
DT 05-JU
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-!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
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TISSUE-Corpora cardiaca;
MEDLINE=98010462; PubMed=9350979; DOI=10.1016/S0167-0115(97)01029-X;
Predel R., Kellner R., Rapus J., Penzlin H., Gade G.;
"Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE-99010462; PubMed-9350979; DOI=10.1016/S0167-0115(97)01029-X; Predel R., Kellner R., Rapus J., Penzlin H., Gade G.; "Isolation and structural elucidation of eight kinins from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: MW=864.10; METHOD=Electrospray; RANGE=1-8;
                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: MW=907.92; METHOD=Electrospray; RANGE=1-8;
NOTE=Ref.1.
-!- SIMILARITY: Belongs to the kinin family.
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Orthopteroidea, Dictyoptera, Blattaria, Blattoidea,
Blattidae, Periplaneta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 8;
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NOTE-Ref.1.
-!- SIMILARITY: Belongs to the kinin family.
-!- SIMILARITY: Belongs to the kinin family.
Amidation; Direct protein sequencing; Neuropeptide.
MOD RES 8 Glycine amide.
SROUENCE 8 AA; 865 MW; C763658449CDC775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        Amidation, Direct protein sequencing, Neuropeptide.
MOD RES 8 Glycine amide.
SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;
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Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Lt. 1.6e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (Rel. 44, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Kinin-5 (Pea-K-5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 36.8%; Score 21; DB Similarity 100.0%; Pred. No. 1.6 3; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (Rel. 44, Created)
                                                                                                                                                                      Regul. Pept. 71:199-205(1997)
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Best Local Similarity
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Best Local Similarity
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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Biochem. J. 131:593-604(1973).
EMBL, M24820; AAA72755.1; -.
NON TER 8
SEQUENCE 8 AA; 969 MW; ECB4
                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=139;
                                                                                                                                                                                                                   Name=PF-50;
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SEQUENCE
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Q37854;
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                                               09R9C4
    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                           Q9R9C4
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PLASMID-group cp32-9, and group cp32-12;
PLASMID-group cp32-9, and group cp32-12;
PLASMID-group cp32-9, and group cp32-12;
MEDLINE-2299654; PubMed=14629041;
Stevenson B., Miller J.C.,
"Intra- and interbacterial genetic exchange of Lyme disease spirochete erp genes generates sequence identity amidst diversity.";
D. Mol. Evol. 57:309-324(2003).
EMBL, AX1422097; AAN17853.1; -...
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MEDLINE=22990544; PubMed=14629041;
Stevenson B., Miller J.C.;
Stevenson B. Miller J.C.;
Intra- and interbacterial genetic exchange of Lyme disease spirochete erp genes generates sequence identity amidst diversity.";
J. Mol. Evol. 57:309-324(2003).
EMBL; AY142092; AAN17873.1; -.
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                                                                                                                                                                                        STRAIN=DN127c19-2; PLASMID=group cp32-9; MEDLINE=22610300; PubMed=12724373; DOI=10.1099/mic.0.26120-0; Miller J.C., Stevenson B.; "Immunological and genetic characterization of Borrelia burgdorferi MapA and EppA proteins."; Microbiology 149:1113-1125(2003).
                                          Borrelia burgdorferi (Lyme disease spirochete).
Plasmid group cp32-9, and Plasmid group cp32-12.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetacese; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid group cp32-5.
Bacteria, Spirochaetes, Spirochaetales, Spirochaetaceae, Borrelia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.8%; Score 21; DB 2; Length 8; 40.0%; Pred. No. 1.6e+06; ative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 1
8 AA; 1042 MW; 1437244330504373 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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9 Aa; 1206 MW; 5A4A244330504373 CRC64;
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PF-50 protein (Fragment).
Name=PF-50;
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Matches 2; Conservative
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SEQUENCE FROM N.A.
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WIIKN 7
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                                                                                                                  NCBI_TaxID=139;
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NON TER
SEQUENCE
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SEQUENCE
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Matches
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086126
AC Q86122
AC Q8612
DT 01-MA
DT 01-MA
DT 01-JU
DE PR-50
GG Bacre
OG Bacre
OG Bacre
OG NCBI
RN [1]
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STRAIN=Sh-2-82; PLASMID=group cp32-4;
STRAIN=Sh-2-82; PLASMID=group cp32-4;
STRAIN=22996544; PubMed=14629041;
Stevenson B., Miller J.C.;
"Intra- and interbacterial genetic exchange of Lyme disease spirochete erp genes generates sequence identity amidst diversity.";
J. Mol. Evol. 57:309-324(2003).
EMBL; AF022479; AAC35438.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=B31; PLASHID=cp32-2;
MEDLINE=98361033; PubMed=9695920;
Stevenson B., Casjens S., Rosa P.;
"Evidence of past recombination events among the genes encoding the Brp antigens of Borrelia burgdorferi.";
Microbiology 144:1869-1879(1998).
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                                                                                                                                                                                                                                       Borrelia burgdorferi (Lyme disease spirochete).
Plasmid cp32-2, and Plasmid group cp32-4.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Borrelia burgdorferi plasmid cp32-2, possible partition proteins, complete cds (PF-50 protein) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 19, Last annotation update)
Coliphage gene of unknown function, 5'end. (Fragment).
Bacteriophage R17.
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9 Aa; 1155 MW; 4E1A244330504373 CRC64;
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9 AA.
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                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
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Best Local Similarity
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MEDLINE=22990544; PubMed=14629041;
MEDLINE=2290544; PubMed=14629041;
Stevenson B., Miller J.C.;
"Intra- and interbacterial genetic exchange of Lyme disease spirochete erp genes generates sequence identity amidst diversity.";
J. Mol. Evol. 57:309-324 (2003).
EMBL; AY142094; AAN17903.1;
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P67787; P08901;
01-NOV-1988 (Rel. 09, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Adipokinetic hormone (Hez-AKH).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopteryota; Arthropoda; Hexapoda; Insecta; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Helicoverpa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid group cp32-8.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
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-!- FUNCTION: This hormone, released from cells in the corpora cardiaca after the beginning of flight, causes release of diglycerides from the fat body and then stimulates the flight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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PROSITE; PS00256; AKH; 1.
Amidation; Direct protein sequencing; Flight; Neuropeptide;
Pyrrolidone carboxylic acid.
MOD_RES
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrrolidone carboxylic acid.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
PF-50 protein (Fragment)
Name-PF-50;
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8 AA; 1042 MW; 1437244337204373 CRC64;
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                                                                                                                                                                                                                                                                                             PRT;
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Best Local Similarity 40.vv,
Best Local Similarity 2; Conservative
                                                                                                                                                                                                                                                                                             PRELIMINARY;
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WILKN 6
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                                            VRNS 8
VRNS
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SEQUENCE
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108GL21
AC 08GL2
AC 08GL2
DT 01-MA
DT 01-MA
DT 01-JU
DE PF-50
GN NOTE
CO NOBL
RN SEQUE
RY STRAI
RY ST
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AKH HEIZE
AKH HEIZE
DT 01-NO
DT 25-OC
DT 25-OC
DE Adipo
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FT MOD_RES 9 9 Glycine amide.

SQ SEQUENCE 9 AA; 1026 MW; 403665A5A1A9D1A7 CRC64;

Query Match 33.3%; Score 19; DB 1; Length 9;

Best Local Similarity 50.0%; Pred. No. 1.6e+06;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps

Qy 2 TVRNSW 7
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] :|| b 3 TFTSSW 8 Search completed: May 19, 2005, 18:25:45 Job time : 175 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 19, 2005, 18:11:02 ; Search time 160 Seconds (without alignments) 21.755 Million cell updates/sec

US-09-867-159A-5 57

1 WTVRNSWDT 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

330156 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* •• Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description			Abb98536 Cysteine		_	Aab76056 Trypanoso	Aaw60399 Tumour ho	Aaw93726 Mouse B16	Aab21816 Murine me	Aae06394 Tumour ho	Aab85132 C. parvum	Abj04066 C parvum	Adq95813 Cryptospo	•	Aab85131 P. vincke	Adq95812 Cryptospo	_			Adr23828 Human CNT	Aar57079 Fasciola	Aau71234 Human MHC	Abg60349 Selective	Adl17323 Human scr	Aab66538 Phage clo	Abg97265 Human leu
ar	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	HACKUS / I	ABB98536	ABJ04065	AAR77352	AAB76056	AAW60399	AAW93726	AAB21816	AAE06394	AAB85132	ABJ04066	ADQ95813	ADH12805	AAB85131	ADQ95812	ADK10416	ADK10223	ADM18218	ADR23828	AAR57079	AAU71234	ABG60349	ADL17323	AAB66538	ABG97265
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* Query Match			100.0	71.9	64.9	63.2	7.9	6.7	7.9	7.9	9.2	5.6	5.6	50.9	50.9	50.9	50.9	50.9	9.1	9.1	7.4	7.4	9.9	9.9	9.6	9.9
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Zinc t. Zinc t. Human HLA bii Human HRB-I TSG-6 Human Human Human Human	Abg34271 Human leu Adk21765 Human 98P Adk02690 Hepatitis Adk07503 Hepatitis Adx330217 Physarum Adc54100 Comman am Ad117066 Phage-dis Aab78541 HIV-2 gp
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# ALIGNMENTS

Antiallergic, antiinflammatory; antiasthmatic; dermatological; allergen; anti-histamine; histamine synthesis inhibitor; allergic hypersensitivity; allergic asthma; allergic rhinitis; cysteine protease protein; enzyme; atopical eczema; epitope. Cysteine protease epitope peptide region, SEQ ID No 5. AAO20571 standard; peptide; 9 AA. 02-JAN-2003 (first entry) AA020571; AA02057 

Dermatophagoides pteronyssinus.

WO200278736-A2.

10-OCT-2002.

28-MAR-2002; 2002WO-FR001098.

30-MAR-2001; 2001FR-00004370. 03-MAY-2001; 2001FR-00005929. 29-MAY-2001; 2001US-00867159.

(ANTI-) ANTIALIS SARL.

Trehin Y;

Terrasse G,

Loria E,

WPI; 2002-750636/81.

Antiallergic compositions containing an anti-histamine, a histamine synthesis inhibitor, and optionally an allergen or nucleic acid coding for the allergen.

Claim 14; Page 11; 32pp; French.

The invention relates to antiallergic compositions containing an antihistamine, a histamine synthesis inhibitor, and optionally an allergen or histamine acid molecule that has at least one polymucleotide sequence coding for the allergen, together with a pharmaceutical carrier. The pharmaceutical composition of the invention is useful as a nonspecific antiallergic treatment, and also useful in the treatment of allergic hypersensitivity, allergic asthma, allergic rethinitis, and also useful and atopical eczema. This sequence represents a peptide of a cysteine protease epitope region relating to the antiallergic

Matches

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The present invention relates to a method of detecting Cryptosporidium in biological and environmental samples, and of diagnosing cryptosporidiosis. This involves obtaining a sample and contacting it with Cryptosporidium GP900, F68 or cryptosporian antigen, antibody, DNA or RNA, or its variant, mutant or fragment. The method is also useful for detecting and identifying individual Cryptosporidium isolates based on the genetic characteristics, and for diagnosis of prior or concurrent Cryptosporidium infection. The present sequence is a C. parvum peptide sequence used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting Cryptosporidium in biological and environmental samples and diagnosis of cryptosporidiosis involves, contacting the sample with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer; amplify; polymerase chain reaction; PCR; Haemonchus contortus; cysteine proteinase; DM.2; DM.3; DM.4; human; DM.4a; DM.5; antigen; vaccine; helminth; parasite; DM.1; ruminant; gastro-intestinal tract.
                                                                                                                                                    Cryptosporidium detection; GP900; P68; cryptopain; cryptosporidiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.9%; Score 41; DB 5; Length 8; 85.7%; Pred. No. 1.8e+06; ive 0; Mismatches 1; Indels
                                                                                                                C parvum crytopain peptide fragment SEQ ID NO: 112.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Gut
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 18; Page 154; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                              Nelson RG,
    ABJ04065 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR77352 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                               14-MAY-2001; 2001WO-US015624.
                                                                                                                                                                                                                                                                                                                                                      06-JUN-2000; 2000US-00588995.
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                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                              Barnes DA,
                                                                                                                                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                               Cryptosporidium parvum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemonchus contortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-566447/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                   WO200194631-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8 AA;
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                                                                            27-SEP-2002
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                                                                                                                                                                                                                                                                         13-DEC-2001
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                                        ABJ04065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to an antiallergic pharmaceutical composition (1) comprising a pharmaceutical carrier containing an active agent combination of at least two of: an allergar, an antihistramine; and a histamine synthesis inhibitor. (1) is used for treating or preventing allergic hypersensitivity reactions, especially allergic asthma, allergic thintis or allergic cacama, in babies, children or adults. The present sequence is a peptide fragment (epitope) of cysteine protease from Dermatophagoides pteronyssinus, which was used as an allergen in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antiallergic composition, useful for preventing and treating e.g. asthma, rhinitis or eczema, containing at least two of allergen, antihistamine and histamine synthesis inhibitor.
                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Antiallergic; antiasthmatic; antiinflammatory; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunotherapy; allergen; allergic hypersensitivity reaction;
allergic asthma; allergic rhinitis; allergic atopic eczema;
                                                                        100.0%; Score 57; DB 5; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 57; DB 5; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         ABB98536 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trehin Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dermatophagoides pteronyssinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 6; 33pp; French.
compositions of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                            Cysteine protease epitope #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-MAY-2001; 2001FR-00005929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001FR-00004370
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ANTI-) ANTIALIS SARL
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                                                                        Query Match
Best Local Similarity
                                                                                                                                                      1 WTVRNSWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cysteine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
                                    Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                      13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR2822709-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                                                                                  ABB98536;
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Loria E,

RESULT 2
ABB98336
ABB98336
ABB98336
AC ABB9
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AC ABB9
AC ABB9
AC ABB9
AC ABB
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Gaps

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05-OCT-1995

RESULT 3

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infections

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The present invention describes a composition (I) which comprises at least one human leukocyte antigen (HLA) binding peptide comprising an isolated, prepared epitope comprising one of 547 8-11 residue amino acid sequences (31), given in AABTS803 to AABT649. (I) has cytostatic, virucide, hepatotropic, antiinflammatory, anti-HIV (human immunofeficiency virus) and protozoacide activities, which can be used in vaccine production and is an inducer of cytotoxic T-cell response. (I) is useful for inducing a cytotoxic T cell response against a preselected antigen in a patient expressing a specific major histocompatibility complex (MHC) class I allele, by contacting cytotoxic T cells (CTLS) from the patient with (I). (I) is useful as a vaccine to treat and/or prevent viral infection and cancer such as prostate cancer, hepatitis B, viral infection and papilloma virus (HPV) infection, cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma acuminatum
                  Composition comprising human leukocyte antigen binding peptide which comprises isolated, prepared epitope useful for treating viral infect such as acquired immunodeficiency syndrome, and cancer.
                                                                                                     Claim 1; Page 46; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9 AA;
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Matches
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                                                                                                                                                                                                                                                                                                                                                             The sequences given in AAR77350-53 are peptides derived from the canonical Haemonchus contortus cysteine proteinase molecule which were used in the design of the primers given in AAQ94240-43. These primers were used in the cloning of coDNA fragments from the cysteine protienase gene, such as DM.1, DM.2, DM.3, DM.4, DM.4a and DM.5 (see also AAQ94246-51). The amplified fragments may be expressed in a recombinant cell for the production of antigens. These antigens may be used in the preparation of a vaccine against helminth parasites in a human or non-human animal
                                                                                                                                                                                                                                                               parasitic nematodes of mammalian gastro-intestinal tract e.g. Haemonchus
                                                                                                                                                                                                                                          Protective helminth parasite antigen - used in vaccine directed against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 8;
                                                                                                                                         Murray J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.9%; Score 37; DB 2; I 71.4%; Pred. No. 1.8e+06;
                                                                                                                                         Smith WD, Redmond D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                (MLCW ) MALLINCKRODT VETERINARY INC
                                                                                                                                                                                                                                                                                                                          Example 16; Fig 15; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; 1
95WO-GB000665
                                                        94GB-00005990
                                        94GB-00005925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 71.4
les 5; Conservative
                                                                                                                                         Knox DP, Smith SK,
                                                                                                                                                                              WPI; 1995-351322/45
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WIVKNSW 8
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                                                                                                                                                                                                    N-PSDB; AAQ94242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8 AA;
                                        25-MAR-1994;
                                                           25-MAR-1994;
                                                                                                                                                                                                                                                                                    contortus.
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Gaps

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63.2%; Score 36; DB 4; Length 9; 57.1%; Pred. No. 1.8e+06; ive 2; Mismatches 1; Indels

| ::||| WIIKNSW 7

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AAW60390-432 represent peptides recovered from mouse melaanomas. The peptides are tumour homing peptides, and are identified by in vivo panning comprises administering a library of diverse peptides to a subject having a tumour, collecting a sample of the tumour, identifying a peptide that homes to the tumour, collecting a sample of normal tissue corresponding to the tumour, and determining that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour homing molecules and their conjugates - useful for, e g. directing linked moiety to tumour containing angiogenic vasculature.
                                                                                                                                                            Tumour homing peptide; in vivo panning; murine melanoma; tumour.
                                                                                                                    Tumour homing peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; Page 80; 105pp; English.
AAW60399 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                           97WO-US016086
                                                                                                                                                                                                                                                                                                                                                                96US-00710067
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ж;
                                                                             24-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasqualini
                                                                                                                                                                                                                                                                                                                                                                                                      (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-207151/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruoslahti E,
                                                                                                                                                                                                                                                                                                                                                                10-SEP-1996;
                                                                                                                                                                                                                                                                                                                         10-SEP-1997;
                                                                                                                                                                                                                                         WO9810795-A2
                                                                                                                                                                                                                                                                                   19-MAR-1998
                                                                                                                                                                                                    Synthetic.
                                       AAW60399;
                    Human leukocyte antigen, HLA, major histocompatibility complex; MHC; cytocoxic T lymphocyte; CTL; human class I MHC; immunogenic; HLA binding peptide; immune response; glycoprotein; cytostatic; virucide; hepatocropic; antiinflammatocy; anti-HIV; vaccine; human immunodeficiency virus; protozoacide; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV; cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS; renal carcinoma; cervical carcinoma; lymphoma; malaria;
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Trypanosoma cruzi HLA-A2 binding peptide.

(first entry)

10-APR-2001

AAB76056;

Southwood S;

WPI; 2001-112389/12

(EPIM-) EPIMMUNE INC Sette A, Sidney J,

29-JUN-1999;

28-JUN-2000; 2000WO-US017842

condyloma acuminatum

Trypanosoma cruzi

WO200100225-A1.

04-JAN-2001.

AAB76056 standard; peptide; 9 AA.

AAB76056 RESULT

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This invention describes novel peptides which home to angiogenic vasculature, specifically of a tumour and which have anti-tumour, anti-inflammatory, anti-angiogenic and anti-arthritic activity. Such molecules are identified by treating a purified NGR receptor with a test compound and identifying compounds that bind specifically to the NGR receptor. The peptides of the invention are inhibitors of angiogenesis and can be used to produce conjugates for delivering agents to angiogenesis or particularly anticancer drugs or an imaging agent, for diagnosis or prognosis. These conjugates may be directed to non-tumour angiogenic vasculature, e.g. that present in inflammatory, regenerating or wounded tissue, e.g. for treatment of macular degeneration, diabetic retinopathy or rheumatoid arthritis. The peptides provide specific targeting to rumours, especially their supporting vasculature, since the NGR receptor is exposed to the circulation only in angiogenic vasculature. Precise targeting should reduce the systemic toxicity of anticancer drugs in the conjugates. Complete killing of all target cells may not be essential since partial denudation of endothelium may result in an occlusive thrombus, and endothelial cells are unlikely to become resistant to anticancer agents nor to lose the targeting receptor. AAM931622-W93809 and
                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecules that home to angiogenic vasculature used as targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour homing peptide; tumour; diagnosis; endothelial cell; melanoma; anglogenic vasculature; anti-tumour; anti-inflammatory; anti-anglogenic; anti-arthritic; NGR receptor; inhibitor; anglogenesis; anticancer drug; prognosis; inflammation; regeneration; wounded tissue; targeting; macular degeneration; diabetic retinopathy; rheumatoid arthritis;
peptide that homes to the tumour is not present in the normal tissue. The tumour homing peptides can be linked to a moiety (e.g. doxorubicin), and used to direct the moiety to a tumour
                                                                                                                                                         Gaps
                                                                                                                                                       .;
0
                                                                                               Score 33; DB 2; Length y;
Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse B16B15b melanoma derived tumour homing peptide 11.
                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example VI; Page 115; 180pp; English.
                                                                                                                                                                                                                                                                                                                             AAW93726 standard; peptide; 9 AA.
                                                                                                                 57.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US018895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-00926914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pasqualini R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   occlusive thrombus; murine
                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-1999 (first entry)
                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for anticancer agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-215158/18.
                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                           1 WTVRNSW 7
                                                                                                                                                                                                                                 1 WTCRASW 7
                                                                             Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-1997;
25-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruoslahti E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9913329-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying
                                                                                                                                                                                                                                                                                                                                                                   AAW93726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus sp
                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                         RESULT 7
                                                                                                                                                                                                                                                                                                           AAW93726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
AAW93843-44 are examples of tumour homing peptides used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer.
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; murine.
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                                                              57.9%; Score 33; DB 2; Length 9; 71.4%; Pred. No. 1.8e+06; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 3; Length 9;
Pred. No. 1.8e+06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pasqualini R, Ruoslahti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Page 96; 118pp; English.
                                                                                                                                                                                                                                                                                                                                             Murine melanoma homing peptide #11
                                                                                                                                                                                                                                               AAB21816 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2000; 2000WO-US001602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00235902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 71.4%; 5; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bredesen DE,
                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BURN-) BURNHAM INST.
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Best Local Similarity
Matches 5; Conserv
                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention
                                                                                                                               1 WTVRNSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WTVRNSW
                                                                                                                                                               WTCRASW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200042973-A2
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                                  Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JAN-1999;
                                                                                                                                                                                                                                                                                                              22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ellerby HM,
                                                                                                                                                                                                                                                                              AAB21816;
                                                                                                Matches
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RESULT

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comprising the cryptopain protein or its fragments are useful for active immunization of animals and humans against Cryptosporidium infection, or for production of passive immune products in admixture with an adjuvant. Cryptopain can be used for prophylactic, therapeutic, diagnostic and detection purposes. The present sequence represents a peptide fragment of the C. parvum cryptopain protein
                                                                                                                                                                                                                                                                             The invention relates to vaccines and cryptopain protein for diagnosis and treatment of Cryptosporidium species infection. Cryptopain protein can be expressed by standard recombinant methodology. The vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting Cryptosporidium in biological and environmental samples and diagnosis of cryptosporidiosis involves, contacting the sample with Cryptosporidium GP900, F68 or cryptopain antigen, antibody, DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cryptosporidium detection; GP900; P68; cryptopain; cryptosporidiosis.
                                                                                                                                                                                                    New vaccines and cryptopain protein for diagnosis and treatment of Cryptosporidium species infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C parvum crytopain peptide fragment SEQ ID NO: 113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.6%; Score 30; DB 100.0%; Pred. No. 1.8; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 154; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelson RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABJ04066 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                     Example 2; Col 19; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-2001; 2001WO-US015624.
                                                                                      96US-0014233P.
                                                             97US-00827171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-2000; 2000US-00588995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barnes DA,
                                                                                                                   CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cryptosporidium parvum.
                                                                                                                                                                             WPI; 2001-388923/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-566447/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRNSW 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200194631-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5 AA;
   US6254869-B1.
                                                             27-MAR-1997;
                                                                                         27-MAR-1996;
                                                                                                                  (REGC ) UNIV
                                03-JUL-2001
                                                                                                                                                Petersen C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petersen C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABJ04066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABJ04066
ID ABJ0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a tunnour homing peptide from mouse B16B15b melanoma. This sequence is useful in the homing of pro-apoptotic
                                                                                                                                 Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; tumour homing molecule; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Novel chimeric prostate-homing pro-apoptotic peptide, used to t
prostate cancer, comprises a prostate-homing peptide linked to
antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                       Ellerby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.9%; Score 33; DB 4; Length 9; larity 71.4%; Pred. No. 1.8e+06; Conservative 0; Mismatches 2; Indels
                                                                                                      Tumour homing peptide #11 from mouse B16B15b melanoma.
                                                                                                                                                                                                                                                                                                                                                                       Bredesen DE,
                                                                                                                                                                                                                                                                                                                                                                       R, Arap W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C. parvum cryptopain protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Page 95; 176pp; English
                AAE06394 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB85132 standard; peptide; 5 AA
                                                                                                                                                                                                                                                                                16-JAN-2001; 2001WO-US001362.
                                                                                                                                                                                                                                                                                                             21-JAN-2000; 2000US-00489582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conjugates of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                       Ruoslahti EI, Pasqualini
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                                                                                                                                                                                                                                                                                                                                          (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-451901/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WTVRNSW
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                                                                                                                                                                                                                       WO200153342-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunization
                                                                         25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-2001
                                                                                                                                                                                                                                                    26-JUL-2001
                                                                                                                                                                cytostatic
                                             AAE06394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB85132;
                                                                                                                                                                                           Mus sp.
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Matches
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Indels Length 5;

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Gaps

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0; Indels

Length 5;

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The present invention relates to a method of detecting Cryptosporidium in biological and environmental samples, and of diagnosing cryptosporidiosis. This involves obtaining a sample and contacting it with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNA, or its variant, mutant or fragment. The method is also useful for detecting and identifying individual Cryptosporidium isolates based on the genetic characteristics, and for diagnosis of prior or concurrent Cryptosporidium infection. The present sequence is a C. parvum peptide sequence used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an antibody produced against and binding to Cryptosporidium antigen, cryptopain. The invention also provides polynucleotides encoding cryptopain which is a cathepsin L-like cysteine proteinase. The antibody is useful for detecting and treating Cryptosporidium infection, for providing passive immunity or for inhibiting existing Cryptosporidium infection antibody is cryptosporidium parvum cryptopain active site fragment comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cryptosporidium infection; antigen; cryptopain;
cathepsin L-like cysteine proteinase; passive immunity; vaccine; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for treating or inhibiting or as vaccine for to provide passive immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.6%; Score 30; DB 8; Length 5; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                   52.6%; Score 30; DB 5; Le
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cryptosporidium parvum cryptopain fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; SEQ ID NO 15; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        ADQ95813 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0014233P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cryptosporium infection.
                                                                                                                                                                                                 Query Match
Best Local Similarity 100.vv
5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cryptopain antibodies,
Cryptosporidium infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-SEP-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 1000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cryptosporidium parvum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved Asn residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petersen C, Huang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-515391/49.
                                                                                                                                                                                                                                                                                   3 VRNSW 7
                                                                                                                                                                                                                                                                                                        1 VRNSW :
                                                                                                                                                                                   Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-1996;
27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6759044-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ95813;
                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                          ADQ95812
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The invention relates to a cellulase (ADH12819) from the abalone Haliotis discus hannai. The cellulase is present in high levels in the liver pancreas of the abalone, particularly the anterior portion. The mature cellulase (EC 3.2.1.4) has an N-terminal sequence given in ADH12801, and has a molecular weight of 66 kD, a pH optimum of 5.5-8.0, an optimum of cellulase (EC 3.2.1.4) has been cellulase at 40 degrees Celsius or below. The invention also encompasses a method for the preparation of the cellulase from abalone internal organs, and further discloses a cDNA sequence (ADH12800) encoding the cellulase. The abalone cellulase is useful in the de-inking and decolouring processes in paper manifacturing, in detergent compositions, and in the manufacture of foods or animal conduction also useful in the degradation of biomass for energy production and for the production of biomass for energy production and for the production of biomass for energy conduction and for the production of biomass for energy production and for the production of biomass for energy collucions and cellulase of the invention is extracted are discarded during processing of the shellfish as a foodstuff. The method of the invention permits helps to reduce the environmental impact of this waste, and permits helps to reduce the environmental impact of cellulase. The present sequence represents an N-terminal peptide fragment of abalone cellulase used to design a degenerate PCR primer in an example of the invention.
                                                                                                                                                                                                                                                                                                                          paper manufacture, detergent, food manfacture, animal fodder,
biomass degradation, energy production, cello-oligosaccharide production,
cellobiose, cellotriose, waste recycling, EC 3.2.1.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel cellulase originating in spiral shells capable of degrading cellulose, useful for producing cell oligosaccharide such as cellobiose and a celltriose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                       Abalone; cellulase; liver pancreas; de-inking; decolouring;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.9%; Score 29; DB 8; Length 7; 57.1%; Pred. No. 1.8e+06; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                 Abalone cellulase Niterminal peptide, SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; SEQ ID NO 6; 21pp; Japanese.
                                                                                                                                         ADH12805 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            Haliotis discus; subsp. hannai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2002; 2002JP-00034852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-FEB-2002, 2002JP-00034852
                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TVRNSWD
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                         1 VRNSW 5
VRNSW 7
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                                                                                                                                                                                                                         11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-2003
                                                                                                                                                                                   ADH12805;
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Matches
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Gaps

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cathepsin L-like cysteine proteinase; passive immunity; vaccine; enzyme
                                                                                                                                                                                                                              Huang J;
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                                                                                                                                                                                                                                                    WPI; 2004-515391/49.
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                                                    Misc-difference
                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8 AA;
                                                                                                                                                                        27-MAR-1996;
27-MAR-1997;
                                                                                                         US6759044-B1
                                                                                                                                                                                                                              Petersen C,
                                                                                                                               06-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to vaccines and cryptopain protein for diagnosis and treatment of Cryptosporidium species infection. Cryptopain protein can be expressed by standard recombinant methodology. The vaccines comprising the cryptopain protein or its fragments are useful for active immunization of animals and humans against Cryptosporidium infection, or for production of passive immune products in admixture with an adjuvant. Cryptopain can be used for prophylactic, therapeutic, diagnostic and detection purposes. The present sequence represents a conserved motif from P. vinckei cysteine proteinase, used for designing degenerate primers for amplifying DNA fragments of C. parvum cryptopain gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                              New vaccines and cryptopain protein for diagnosis and treatment of Cryptosporidium species infection.
                                                                                                     Cryptosporidium; infection; cryptopain; antiparasitic; vaccine; immunization; cysteine proteinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.9%; Score 29; DB 4; Length 8; 57.1%; Pred. No. 1.8e+06; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cryptosporidium infection; antigen; cryptopain;
                                                                                  P. vinckei cysteine proteinase conserved motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cryptosporidium parvum cryptopain fragment #2.
                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                  label= Val or Ile
                                                                                                                                                                                                       /label= Lys or Arg
                  AAB85131 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Col 19; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADQ95812 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                        97US-00827171
                                                                                                                                                                                                                                                                                            96US-0014233P
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                        Huang J;
                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-388923/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                        Plasmodium vinckei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WTVRNSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WIXXNSW
                                                                                                                                                                       Misc-difference
                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8 AA;
                                                                                                                                                                                                                             US6254869-B1
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                                                                                                                                                                                                                                                                                                                                       Petersen C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-SEP-2004
                                                             22-AUG-2001
                                                                                                                                                                                                                                                  03-JUL-2001
                                       AAB85131;
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         AAB8513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating or inhibiting or as vaccine for to provide passive immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; SEQ ID NO 14; 33pp; English.
                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: May 19, 2005, 18:22:51
Job time : 168 secs
                                                                                                        /label= Val, Ile
                                                                                                                                                                /label= Lys, Arg
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97US-00827171.
                                                                                                                                                                                                                                                                                                                                          20-JUN-2000; 2000US-00598062
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Similarity 57.1%;
4; Conservative 0
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Cryptosporidium infection,
to Cryptosporium infection.
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Cryptosporidium parvum.
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Sequence 116, App
Sequence 116, App
Sequence 116, App
Sequence 116, App
Sequence 25, App
Sequence 24, App
Sequence 24, App
Sequence 28, App
Sequence 286, App
Sequence 286, App
Sequence 130, App
Sequence 130, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                            May 19, 2005, 18:25:53 ; Search time 132 Seconds (without alignments) 22.807 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/VEOT_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/NEOT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/NEOT_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/NEOT_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
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12: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/NEOM_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-264-374-116
US-10-264-374-116
US-10-375-992-116
US-10-375-992-116
US-10-38-348-25
US-09-834-765-155
US-10-363-204-24
US-10-100-082-286
US-10-100-082-286
US-10-024-652-981
US-10-048-652-981
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                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                        1434725 seqs, 334507595 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                  Run on:
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No.
                                                                                                                                                                                                                     Title:
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	Sequence 30, Appl	235,	353	649	119	30,	Sequence 235, App	353	649	30,	235	353	649	677	16,	164	184,		664,	664,	664,	664,	664,	664,	17,	471,	626,	628,	627,	Sequence 129, App	133,
-10-888-348-2	US-09-793-451-30	US-09-793-451-235	-451-	-60-	US-09-942-052-119	-10 - 283 - 72	-10 - 283	-10 - 283	-10-	-10	-10-283-903-	US-10-283-903-353	-10-	US-10-808-187-677	US-10-190-082-16	-10-351-	-10-	US-10-334-726-295	-10-609-217	-10-632-388-6	US-10-651-723-664	2	-10-666-	-10-653-048-6	US-10-705-195-17	US-10-714-564A-471	-10-	-10-072-	-10-072-602B-6	US-10-190-082-129	US-10-190-082-133
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45.6	43.9	43.9	43.9	43.9	43.9	43.9	43.9	43.9	43.9	43.9	43.9	43.9	43.9	43.9	42.1	24 42.1 6			42.1	42.1	42.1	42.1	42.1	42.1	40.4	40.4	40.4	40.4	40.4	23 40.4	40.4
14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Sequence 1.37—2.

Sequence 5. Application US/09867159A

Publication No. US20030104013A1

GENERAL INFORMATION:

JENURAL INFORMATION:

TITLE OF INVENTION: Anti-allergic pharmaceutical composition containing at least one TITLE OF INVENTION: and at least one anti-histamine compound

TITLE OF INVENTION: Anti-allergic pharmaceutical composition containing at least one TITLE OF INVENTION: and at least one anti-histamine compound

TITLE OF INVENTION: Anti-allergic pharmaceutical composition containing at least one TITLE OF INVENTION: Anti-allergic pharmaceutical compound

FILE REFERENCE: B112812US-anti-alis

CURRENT FILING DATE: 2001-05-29

PRIOR APPLICATION NUMBER: FR01/04370

PRIOR APPLICATION NUMBER: FR01/0529

PRIOR PILING DATE: 2000-05-03

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.1

SEQ ID NO 5

LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : .LOCATION: (1)..(9)
; OTHER INFORMATION: Comprises epitope from cystine protease. US-09-867-159A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 57; DB 10;
100.0%; Pred. No. 1.3e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Dermatophagoides pteronyssinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
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Sequence 116, Application No. US2030113320A1

GENERAL INFORMATION:

APPLICANT: Rucelaht; Erkki

APPLICANT: Rucelaht; Erkki

APPLICANT: Pasqualini, Renata

TITLE OF INVENTION: MOICCULES That Home to Angiogenic Vasculature Using

TITLE OF INVENTION: Same

FILE REFERENCE: P-LJ 3203

FILE REFERENCE: P-LJ 3203

CURRENT APPLICATION NUMBER: US/10/264,374

CURRENT APPLICATION NUMBER: US/09/139,802

PRIOR APPLICATION NUMBER: US/09/139,802

PRIOR APPLICATION NUMBER: 08/26,914

PRIOR FILING DATE: 1998-09-10

PRIOR FILING DATE: 1996-09-10

NUMBER OF SEQ ID NOS: 226

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 116

LENGTH: PATENTINE OF THE OFFICE OFFIC
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US-10-264-374-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                    GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Raequalini, Renata
APPLICANT: Wadih, Arap
APPLICANT: Bredesen, Dale E.

APPLICANT: Bredesen, Dale E.

APPLICANT: Bleeby, H. Michael
TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
TITLE OF INVENTION: Pro-Apoptotic Activity
FILE REFERENCE: P-LJ 3844

CURRENT FILING DATE: 2001-01-17

PRICA APPLICATION NUMBER: US 09/489,582

PRICA REPLICATION NUMBER: US 09/489,582

PRICA REPLICATION NUMBER: 2000-01-21

NUMBER OF SEQ ID NOS: 235

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 116

LENGTH: 9
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Pred. No. 1.3e+06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
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Pred. No. 1.3e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: synthetic peptide US-09-765-086-116
Sequence 116, Application US/09765086
Patent No. US20010046498A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.9%;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 57.9
Best Local Similarity 71.4
Matches 5; Conservative
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US-10-264-374-116
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1 WTCRASW 7

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Sequence 116, Application US/10264374

Publication No. US20040096441A9

GENERAL INFORMATION:
APPLICANT: Rubelahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: MGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Same
FILE REFERENCE: P-LJ 3203
CURRENT APPLICATION UNMBER: US/10/264,374
CURRENT APPLICATION UNMBER: US/09/139,802
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 08/926,914
PRIOR FILING DATE: 1997-09-10
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Sequence 116, Application US/10375992
Publication No. US20030152578A1
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
Pasqualini, Renata
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
Derived Therefrom, and Methods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
CONNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
WINDITH TREADABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-375-992-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (619) 535-9001
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SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 57.9
Best Local Similarity 71.4
Matches 5; Conservative
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GENERAL INFORMATION:

APPLICANT: Pia M. Challita-Eid
APPLICANT: Pia M. Challita-Eid
APPLICANT: Arbur B. Raiteno
APPLICANT: Arbur B. Raiteno
APPLICANT: Arbur B. Raiteno
APPLICANT: Arbur B. H. Afar
APPLICANT: Arbur B. H. Afar
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT:
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT:
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT:
TITLE OF INVENTION: AND DETECTION OF CANCER
FILE REFERENCE: 129.6USU1
CURRENT FALLING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/197,647
MIMMED OF GEO TE NOT CONTINUED.
                                                                                             US-10-888-348-25
; Sequence 25, Application US/10888348
; Publication No. US20050064555A1
; Publication No. US20050064555A1
; Publication No. US2005006455A1
; APPLICANT: Marshall, Shannon
; APPLICANT: Barbosa, Maria
; TITLE OF INVENTION: CILLARY NEUROTROPHIC FACTOR VARIANTS
; FILE REFRENCE: 34431/US
; CURRENT APPLICATION NUMBER: US/10/888,348
; CURRENT APPLICATION NUMBER: US 60/485,941
; PRIOR PLILING DATE: 2003-07-09
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: Patentin Version 3.3
; SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 27; DB 9; ]
Pred. No. 1.3e+06;
0; Mismatches 3
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Pred. No. 1.3e+06;
1; Mismatches 2
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-834-765-155
; Sequence 155, Application US/09834765
; Patent No. US20020055478A1
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Similarity 62.5%;
5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-888-348-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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Best Local Similarity
Matches 5; Conserv
              1 WTCRASW 7
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US-10-363-204-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 116, Application US/10375992
Publication No. US20040131623A9
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
Pasqualini, Renata
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
Derived Therefrom, and Methods of Using Same
                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide
US-10-264-374-116
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/375,992
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                            Score 33; DB 15; Length 9;
Pred. No. 1.3e+06;
                                                                                                                                                                                                                                                                                                                                                       2; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2725
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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APPLICATION NUMBER: US/08/926,914
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-375-992-116
PRIOR APPLICATION NUMBER: 08/710,067
PRIOR FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 116
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (619) 535-9001
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     57.9%;
71.4%;
                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                          Query Match 57.9
Best Local Similarity 71.4
Matches 5; Conservative
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US-10-375-992-116
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Gaps

. 0

Length 9; Indels ö

Gaps

. 0

3; Indels Length 9;

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APPLICANT: Afar, Daniel E.H.
APPLICANT: Afar, Daniel E.H.
APPLICANT: Afar, Daniel E.H.
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Abacbovits, Aya
TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Detection of Cancer
FILE REFERENCE: 51158-20025.00
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/256,210
PRIOR FILING DATE: 2002-12-15
               APPLICANT: Jakobovite, Aya
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
FILE REFERENCE: 51158-20025.00
CURRENT APPLICATION NUMBER: US/10/024,652
PRIOR PILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 2598
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 130
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                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 45.6%; Score 26; DB 15; Length 9; Best Local Similarity 62.5%; Pred. No. 1.3e+06; Matches 5; Conservative 0; Mismatches 3; Indels
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Pred. No. 1.3e+06;
0; Mismatches 3
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 981
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 134, Application US/10482284A Publication No. US20050019344A1 GENERAL INFORMATION: APPLICANT: KHANNA, Rajiv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 981, Application US/10024652
Publication No. US20030219738A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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ilarity 62.5%;
Conservative
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US-10-024-652-981
                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
....a 5; Conserve
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US-10-024-652-981
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               GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REFERENCE: 005774.P003PCT
CURRENT APPLICATION NUMBER: US/10/363,204
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 251
SOFTWARE: Patentin version 3.1
SEQ ID NO 24
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APPLICANT: Sidhu, Sachdev S.
APPLICANT: Aldhu, Sachdev S.
TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
FILE REFREENCE: P1905R1
CURRENT PILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/303,634
PRIOR APPLICATION NUMBER: US 60/303,634
NUMBER FO SEQ ID NOS: 683
SEQ ID NO 286
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                                                                                                                                                                                                                                                                                                        Sequence 286, Application US/10190082
Publication No. US20030148264Al
GENERAL INFORMATION:
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Publication No. US20030219738A1
GENERAL INFORMATION:
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Mitchell, Steve Chappell
Levin, Elana
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E.H.
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ORGANISM: Artificial sequence
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Publication No. US20040170955A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic US-10-190-082-286
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Best Local Similarity 80.0
Matches 4; Conservative
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US-10-024-652-130
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APPLICANT:
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APPLICANT:
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APPLICANT: Aya Jakobovite
TITLE OF INVENTION: 10322D6: TISSUE SPECIFIC PROTEIN HIGHLY
TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129-1302U2
CURRENT APPLICATION NUMBER: US/09/793,451
CURRENT PILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/184,558
PRIOR FILING DATE: 2000-02-34
PRIOR FILING DATE: 2000-07-13
PRIOR FILING DATE: 2000-07-13
SOFTWARE: FABLEEQ for Windows Vergion 4.0
SEQ ID NO 30
FEACTH. 0
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Job time : 133 secs
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ORGANISM: homo sapiens
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Best Local Similarity
Matches 3; Conserv
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               APPLICANT: WALKER, Susan J.

TITLE OF INVENTION: Novel human cytomegalovirus (HCMV) cytotoxic T cell epitopes,
TITLE OF INVENTION: wovel human cytomegalovirus (HCMV) cytotoxic T cell epitopes,
TITLE OF INVENTION: uses therefore
FILE REFERENCE: 47-203
FILE REFERENCE: 47-203
FILE REFERENCE: 47-203
FILE OF INVENTION: UNMBER: US/10/482,284A
CURRENT RILING DATE: 2003-12-29
PRIOR APPLICATION NUMBER: AU PR5931
PRIOR APPLICATION NUMBER: AU PR5931
NUMBER OF SEQ ID NOS: 318
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: human cytomegalovirus pp65; OTHER INFORMATION: epitope peptide
US-10-482-284A-134
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Sequence 24, Application US/1088348

Sequence 24, Application US/1088348

Publication No. US20050064555A1

GENERAL INFORMATION:

APPLICANT: Marehall, Shannon

APPLICANT: Barbosa, Maria

TITLE OF INVENTION: CILIARY NEUROTROPHIC FACTOR VARIANTS

FILE REFERENCE: 34431/US

CURRENT APPLICATION NUMBER: US/10/888,348

CURRENT PILING DATE: 2004-07-09

PRIOR APPLICATION NUMBER: US 60/485,941

PRIOR APPLICATION NUMBER: US 60/528,229

PRIOR FILING DATE: 2003-12-08

NUMBER OF SEQ ID NOS: 165

SOFTWARE: Patentin Version 3.3

SEQ ID NO 24

LENGTH: 9
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ORGANISM: human cytomegalovirus pp150 CTL epitope peptide
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Gazelle S. Rastegar
Steve Chappell Mitchell
Rene S. Hubert
Pia M. Challita-Eid
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ELKINGTON, Rebecca A.
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APPLICANT: Daniel E.H. Afar
APPLICANT: Gazelle S. Rasteg
APPLICANT: Steve Chappell Mi
APPLICANT: Rene S. Hubert
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Best Local Similarity 80.0
Local 4; Conservative
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US-10-888-348-24
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LENGTH: 9
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Sequence 112, App
Sequence 116, App
Sequence 116, App
Sequence 116, App
Sequence 113, Appl
Sequence 113, Appl
Sequence 14, Appl
GENERAL INFORMA
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42, Appl
77, Appl
1488, Ap
1648, Ap
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                                                                     May 19, 2005, 18:17:01; Search time 41 Seconds (without alignments) 16.386 Million cell updates/sec
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/cgn2_6/ptodata1/jaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-139-802-116
US-09-26-914-116
US-08-926-914-116
US-08-926-914-116
US-08-926-914-116
US-09-588-062-14
US-09-598-062-14
US-09-598-062-14
US-08-924-695A-79
US-08-924-695A-79
US-08-924-695A-79
US-08-924-695A-77
US-08-92-79B-1488
US-09-92-93B-34
US-08-453-076E-78
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3 US-09-082-279B-1486 3 US-09-082-279B-1489 3 US-09-082-279B-1499 3 US-09-31S-304B-1562 3 US-09-31S-304B-1639 3 US-09-31S-304B-1639 3 US-09-31S-304B-1639 3 US-09-31S-304B-1640 3 US-09-31S-304B-1640 3 US-09-31S-304B-1640 4 US-09-31S-304B-1689 4 US-09-834-784-1486 4 US-09-834-784-1486 4 US-09-834-784-1486 4 US-09-834-784-1486 4 US-09-834-784-1486 4 US-09-834-784-1489 4 US-09-834-784-1489 4 US-09-834-784-1499	LIGNMENTS 95A TECTION OF CRYPTC FOR DIAGNOSIS OF 71 61 51			US/09139802 ki
2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3	ALIL  18-09-588-995A-112  Sequence 112, Application US/09588995.  Sequence 112, Application US/09588995.  GENERAL INFORMATION: APPLICANT: BARNES, DEBRA A. APPLICANT: BARNES, DEBRA A. APPLICANT: GUT, JIRI TITLE OF INVENTION: METHODS FOR DETE TITLE OF INVENTION: METHODS FOR DETE TITLE OF INVENTION: INFECTIONS FILE REFERENCE: 480.19-5 CURRENT APPLICATION NUMBER: US/09/58 CURRENT FILING DATE: 1997-03-27 PRIOR APPLICATION NUMBER: 08/928,361 PRIOR FILING DATE: 1997-03-27 PRIOR FILING DATE: 1996-08-12 PRIOR FILING DATE: 1996-04-03 NUMBER OF SEQ ID NOS: 115 SEQ ID NO 112 LENGTH: 8 TYPE PRI TYPE PATURENT NUMBER: 08/15,751 PRIOR FILING DATE: 1996-04-03 NUMBER OF SEQ ID NOS: 115 SEQ ID NO 112 LENGTH: 8 TYPE: PRT TYPE PRIOR TYPE PRI ORGANISM: CTYPTOSPOTIGIUM PARVUME: FRANURE: FR	MOD_RES (3) CRMATION: L or A-112 A-112 Similarity 85 6; Conservativ	1 WTVRNSW 7	SULT 209-139-802-116 Sequence 116, Application US/09139802 Sequent No. 6180084 GENERAL INFORMATION: APPLICANT: Ruoslahti, Erkki
0 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1	RESULT 1 US-09-588-995A-112 Sequence 112, Appli, Patent No. 6514697 GENERAL INFORMATION APPLICANT: PETERSE, APPLICANT: PETERSE, APPLICANT: BARNES APPLICANT: GT, J TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION FILE REPERENCE: 48 CURRENT APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR PELING DATE: PRIOR FILING DATE: PRIO	; NAME/KEY: MOD ; LOCATION: (3) ; OTHER INFORMAL US-09-588-995A-11 Query Match Best Local Simi	čo da	RESULT 2 US-09-139-802-116 ; Sequence 116, Applic; Patent No. 6180084 ; GENERAL INFORMATION: ; APPLICANT: Ruoslaht

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APPLICANT: Rucelaht; Erkki

GENERAL INFORMATION:

APPLICANT: Rucelaht; Erkki

APPLICANT: Rucelaht; Erkki

APPLICANT: Rucelaht; Erkki

TITLE OF INVENTION: MGR Receptor and Methods of Identifying Tumor Homing

TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using

TITLE OF INVENTION: Same

FILE REFERENCE: P-LJ 3203

CURRENT FILING DATE: 2000-09-11

PRIOR PILING DATE: 2000-09-11

PRIOR APPLICATION NUMBER: 08/926,914

PRIOR APPLICATION NUMBER: 08/710,067

PRIOR PILING DATE: 1996-09-10

NUMBER OF SEQ ID NOS: 226

SOFTWARE: Patentin Ver. 2.0

LENGTH: 9
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               TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using TITLE OF INVENTION: Same FILE OF INVENTION: Same FILE REPERBNCE: P-LJ 3203
CURRENT APPLICATION NUMBER: US/09/139,802
CURRENT PILING DATE: 1996-08-25
EARLIER APPLICATION NUMBER: 08/226,914
EARLIER FILING DATE: 1997-09-10
RARLIER FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PATENTION OF SEQ ID NOS: 226
SOFTWARE: PATENTION OF SEQ ID NOS: 226
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-139-802-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-659-786-116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.9%; Score 33; DB 3; Length 9; 71.4%; Pred. No. 4.1e+05;
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Pred. No. 4.1e+05;
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US-08-926-914-116
; Sequence 116, Application US/08926914
; Patent No. 6576239
; GENERAL INFORMATION:
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APPLICANT: Pasqualini, Renata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 71.*
Best Local Similarity 71.*
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Matches 5; Conservative
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US-09-659-786-116
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TITLE OF INVENTION: PEPTIDES, DNA AND RNAS FOR PROPHYLAXIS,
TITLE OF INVENTION: TREATMENT, DIAGNOSIS AND
TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, USRNY, JONES & BIK A
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Allo
COUNTRY: United States of America
ZIP: 94306-1840
ZIP: 94306-1840
ZIP: 94306-1840
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
NUMBER OF SEQUENCES: 199
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/926,914
FILING DATE: 10-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 9-LJ 2725
TELECOMMULCATION NUMBER: P-LJ 2725
TELECOMMULCATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9049
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: WINDOWS
SOFTWARE: Wordperfect 6.0a WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,171B
FILING DATE:
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
SEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 15, Application US/08827171B ; Patent No. 6254869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: CAROLYN PETERSEN
APPLICANT: JIN-XING HUANG
                                                                                                                                                                                                                       United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: both
MOLECULE TYPE: peptide
                                                                                                                                               STREET: 4370 La Jol
CITY: San Diego
STATE: California
COUNTRY: United Sta
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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Best Local Similarity
Matches 5; Conserv
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US-08-827-171B-15
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GENERAL INFORMATION:
APPLICANT: CAROLYN PETERSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 385 Sherma
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VRNSW 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-598-062-15
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100.0%; Pred. No. 4.1e+05;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.6%; Score 30; DB 3; Length 5; 100.0%; Pred. No. 4.1e+05; tive 0; Mismatches 0; Indels
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,233
FILING DATE: March 2', 1996
ATTORNEY/ACENT INFORMATION:
NAME: Hana Verny
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: (HV)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 324-1678
INFORMATION FOR SEQ ID NO: 15:
LENGRATION FOR SEQ ID NO: 15:
LENGRATION FOR SEG ID NO: 15:
LENGRATION FOR FER INFORMATION FO
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; Patent No. 6759044
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; ORGANISM: Cryptosporidium parvum
US-09-588-995A-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.6
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: peptide US-08-827-171B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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US-09-588-995A-113
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TITLE OF INVENTION: CRYPTOPAIN VACCINES, ANTIBODIES, PROTEINS, PEPTIDES, DNA AND RNAS FOR PROPHYLAXIS, TREATMENT, DIAGNOSIS AND DETECTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/08827171B
Patent No. 6254869
GENERAL INFORMATION:
APPLICANT: CARCLYN PETERSEN
APPLICANT: JIN-XING HUANG
TITLE OF INVENTION: REPTIOES, DIA AND RNAS FOR PROPHYLAXIS,
TITLE OF INVENTION: DETECTION OF
TITLE OF INVENTION: DETECTION OF
TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM
MANAGED OF INVENTION: CRYPTOSPORIDIUM PARVUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                 NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: PETERS, VERNY, JONES & BIK A
STREET: 395 Sherman Avenue, Suite 6
CITY: Palo Alto
STATES: California
COUNTRY: California
COUNTRY: California
CONPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 KD storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 KD storage
COMPUTER: PC
OPERATING SYSTEM: WINDOWS
SOFTWARE: Wordperfect 6.0a WINDOWS
SOFTWARE: Wordperfect 6.0a WINDOWS
SOFTWARE: Wordperfect 6.0a WINDOWS
SOFTWARE: WORDPER: US/09/598,062
FILING DATE: COUNCOMP
FILING DATE: COUNCOMP
FILING DATE: ADMINOMP
FILING DATE: AURICOMP
APPLICATION NUMBER: 60/014,233
FILING DATE: MARCH 27, 1996
ATTORNEY AGENT INCRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.6%; Score 30; DB 4; Length 5; 100.0%; Pred. No. 4.1e+05; Live 0; Mismatches 0; Indels
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CORRESPONDENCES: 16
CORRESPONDENCE ADDRESS: 18
ADDRESSEE: PETERS, VERNY, JONES & BIK A STREET: 385 SHERMAN AVENUE, SUITE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: (HV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (415) 324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 324-1678
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 5; Conservative
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Gaps

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RESULT 10
US-08-706-741B-79
; Sequence 79, Application US/08706741B
; Sequence 79, Application US/08706741B
; Parent No. 5955593
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITT: ST. LOUIS
; STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
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                                                                                                                                                                                                                                                                                                                                                                       50.9%; Score 29; DB 4; Length 8; 57.1%; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FAPLICATION NUMBER: US/08/706,741B
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.5%; Score 26.5; DB 2; 55.6%; Pred. No. 4.1e+05; tive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                       IDENTIFICATION METHOD:
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                    APPLICATION NUMBER: 60/014,233
FILING DATE: March 27, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                NAME: Hana Verny
REGISTRATION NUMBER: 30,518
REPERENCE/DOCKET NUMBER: (HV)
TELECOMMINICATION INFORMATION:
TELEPHONE: (415) 324-1677
TELEFAX: (415) 324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTY: 034

ZIP: 63146

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 96;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WT-VRNSWD 8
                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || : |||
WTRIIQSWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WTVRNSW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 WIXXNSW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-706-741B-79
                                                                                                                                                                                                                                                                                                                         US-09-598-062-14
                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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JIN-XING HUNG
JIN-XING HUNG
TITLE OF INVENTION: CRYPTOPAIN VACCINES, ANTIBODIES, PROTEI
PEPTIDES, DNA AND RNAS FOR PROPHYLAXIS,
TREATMENT, DIAGNOSIS AND
DETECTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
ADDRESSE: PETERS, VERNY, JONES & BIK A
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto STATE: California
COUNTRY: United States of America
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.9%; Score 29; DB 3; Length 8; Best Local Similarity 57.1%; Pred. No. 4.1e+05; Matches 4; Conservative 0; Mismatches 3; Indels
COUNTRY: United States of America
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: PC
OPERATING SYSTEM: WINDOWS
SOFTWARE: Wordperfect 6.0a WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/598,062
FILING DATE: 20-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/827,171
                                                                                                                      OPERATING SYSTEM: WINDOWS
SOFTWARE: WORDPERFOCE 6.0a WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,171B
                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,233
FILING DATE: March 27, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hana Verny
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: (HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-1678
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Xaa at 4 is Val/Ile
NAME/KEY: Xaa at 5 is Lys/Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: CAROLYN PETERSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD:
) OTHER INFORMATION:
US-08-827-1718-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WTVRNSW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 WIXXNSW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-09-598-062-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION
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Gaps

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Gaps

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Sequence 77, Application US/08706741B
Fatent No. 595553
GENERAL INPORMATION:
APPLICANT: KORNWER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEB: HOWELL & HAPERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                            Score 24.5; DB 2; Length 9; Pred. No. 4.1e+05; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
-APPLICATION NUMBER: US/08/706,741B FILING DATE: 09-SEP-1996 CLASSIFICATION:
-ATORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.0%; Score 24.5; DB 2; 55.6%; Pred. No. 4.1e+05; tive 0; Mismatches 3;
               ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMONICATION INFORMATION:
TELEPRAN: (314) 727-5188
TELEPRAN: (314) 727-5188
INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                 43.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide US-08-706-741B-77
                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WKEHNRSWD 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WTVRN-SWD 8
                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WTVRN-SWD
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 63146
                                                                                                                                                                                                                                                                                                                                                                   US-08-733-505A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-706-741B-77
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US-08-733-505A-42

is Sequence 42, Application US/08733505A

is General No. 585445

is GENERAL INFORMATION:

APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF

TITLE OF INVENTION: BCL-Z ASSOCIATED CELL DEATH REGULATOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAFERKAMP, L.C.

STREET: 7733 FORSYTH BLVD., SUITE 1400

CITY: ST. LOUIS

STRETE: MISSOURI
     US-08-924-695A-79

US-08-924-695A-79

Sequence 79, Application US/08924695A

Patent No. 5998893

GRNERAL INFORMATION:

APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST

OURRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAFERKAMP, L.C.

STREET: 77-33 FORSYTH BLVD., SUITE 1400

CITY: ST. LOUIS

STATE: MISSOURI

COMPUTER: RADABLE FORM:

MEDIUM TYPE: FLODY disk

COMPUTER: IBM PC COMPALIDLE

COMPUTER: IBM PC COMPALIDLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: BATCHIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/924,695A

FILING DATE: 09-SEP-1997

CLASSIFICATION ONALD R.

REGISSTRICATION NUMBER: 35,197

REFERENCE/DOCKET UNFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.5%; Score 26.5; DB 2; Length 9; 55.6%; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
INFORTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WT-VRNSWD 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WTRIIQSWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-924-695A-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
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US-09-082-279B-1488

1 WKEHNRSWD 9

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Query Match 42.1%; Score 24; DB 3; Length 8;

Best Local Similarity 42.9%; Pred. No. 4.18+05;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTVRNSW 7

| | | ::| |
Db 1 WDVFSNW 7

Search completed: May 19, 2005, 18:27:15
Job time: 42 secs
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